IN THE SPECIFICATION

On page 1 of the specification, please amend the title beginning on line 2 as follows:

~~Novel Genes Encoding Proteins Having Prognostic, Diagnostic, Preventive, Therapeutic, And Other Uses~~ Anti-Tango294 Antibodies and Uses Thereof

On page 1 of the specification, please amend the Cross-Reference to Related Applications beginning on line 6 as follows:

This application is a continuation-in-part of U.S. Application serial number 09/479,249, filed on January 7, 2000, now abandoned, and a continuation-in-part of U.S. Application serial number 09/559,497, filed on April 27, 2000, now abandoned.

This application is also a continuation-in-part of U.S. Application serial number 09/578,063, filed on May 24, 2000, now U.S. Patent No. 6,764,677, which is a continuation-in-part of U.S. Application serial number 09/333,159, filed on June 14, 1999, now U.S. Patent No. 7,033,780.

This application is also a continuation-in-part of U.S. Application serial number 09/596,194, filed on June 16, 2000~~July 14, 2000~~, now abandoned, which is a continuation-in-part of U.S. Application serial number 09/342,364, filed on June 29, 1999, now abandoned.

This application is also a continuation-in-part of U.S. Application serial number 09/608,452, filed on June 30, 2000, now abandoned, which is a continuation-in-part of U.S. Application serial number 09/393,996, filed on September 10, 1999, now abandoned.

This application is also a continuation-in-part of U.S. Application serial number 09/602,871, filed on June 23, 2000, now abandoned, which is a continuation-in-part of U.S. Application serial number 09/420,707, filed on October 19, 1999, now abandoned.

Please amend the Brief Description of the Drawings section beginning on line 8 of page 21 of the specification as follows:

BRIEF DESCRIPTION OF THE DRAWINGS

~~Figure 1 comprises Figures 1A through 1I. The nucleotide sequence (SEQ ID NO: 1) of a cDNA encoding the human TANGO 416 protein described herein is listed in Figures 1A through 1I. The open reading frame (ORF; residues 376 to 3780; SEQ ID NO: 2) of the cDNA is indicated by nucleotide triplets, above which the amino acid sequence (SEQ ID NO: 3) of human TANGO 416 is listed.~~

~~Figure 2 comprises Figures 2A through 2I. The nucleotide sequence (SEQ ID NO: 31) of a cDNA encoding the human TANGO 416 protein described herein is listed in Figures 2A through 2I. The open reading frame (ORF; residues 376 to 3777; SEQ ID NO: 32) of the cDNA is indicated by nucleotide triplets, above which the amino acid sequence (SEQ ID NO: 33) of human TANGO 416 is listed.~~

Figure 1 [[3]] is a hydrophobicity plot of the embodiment of human TANGO 416 protein listed in SEQ ID NO:3~~Figure 1~~. In the hydrophobicity plots disclosed herein, the locations of cysteine residues ("Cys") and potential N-glycosylation sites ("Ngly") are indicated by vertical bars and the predicted extracellular ("out"), intracellular ("ins"), or transmembrane ("TM") portions of the protein backbone are indicated by a horizontal bar. Relatively hydrophobic regions of the protein are above the dashed horizontal line, and relatively hydrophilic regions of the protein are below the dashed horizontal line.

Figure 2A-2H[[4]] is an alignment of a portion of the TANGO 416 cDNA sequence ("T416"; residues 1651-4000 of SEQ ID NO: 1) with a human testis cDNA clone having GenBank accession number AL137471 ("AL137471"; SEQ ID NO: 40). This alignment indicates that the two nucleotide sequences are about 98.6% identical over the overlapping region. The alignment was made using the ALIGN software (BLOSUM62 scoring matrix, gap opening penalty 12, gap extension penalty 4, frameshift gap penalty 5). In the alignments in this disclosure, similar residues are indicated by ".", and identical residues are indicated by ":" or "|".

Figure 3A-3O[[5]] is an alignment of a portion of the TANGO 416 ORF nucleotide sequence ("T416"; residues 1-3405 of SEQ ID NO: 2) with the ORF nucleotide sequence ("m-PC"; SEQ ID NO: 41) of murine protocadherin (sometimes designated vascular endothelial cadherin-2 or mVE-cad-2). This alignment indicates that the two nucleotide sequences are about 55.4% identical over the overlapping region. The alignment was made using the ALIGN software (BLOSUM62 scoring matrix, gap opening penalty 12, gap extension penalty 4, frameshift gap penalty 5).

Figure 4A-4E[[6]] is an alignment of a portion of the TANGO 416 protein amino acid sequence ("T416"; residues 1-1135 of SEQ ID NO: 3) with the amino acid sequence ("m-PC"; SEQ ID NO: 42) of murine protocadherin. This alignment indicates that the two amino acid sequences are about 32.8% identical over the overlapping region. The alignment was made using the ALIGN software (BLOSUM62 scoring matrix, gap opening penalty 12, gap extension penalty 4).

~~Figures 7A through 7D depict a cDNA sequence of human TANGO 457 (SEQ ID NO: 51) and the predicted human TANGO 457 amino acid sequence encoded by the sequence (SEQ ID NO: 53). The open reading frame of TANGO 457, comprises nucleotide 149 to nucleotide 1243 of SEQ ID NO: 51 (SEQ ID NO: 52).~~

Figure 5[[8]] depicts a hydrophobicity plot of human TANGO 457.

Figures 6A-6D~~9A through 9D~~ depict a local alignment of the nucleic acid of human TANGO 457 shown in SEQ ID NO: 51 and a portion of the nucleotide sequence of human chromosome 11p14.3 PAC clone pDJ239b22, from nucleic acids 121077 to 122478 (SEQ ID NO: 61; accession number AC003969). In the alignment, the TANGO 457 sequence is the top strand, and the 11p14.3 PAC clone pDJ239b22 sequences is on the bottom. The alignment shows that there is 100% nucleotide sequence identity between the TANGO 457 sequence of SEQ ID NO: 51 and human chromosome 11p14.3 PAC

clone pDJ239b22, from nucleotides 908 to 2305 of TANGO 457. This alignment was performed using the ALIGN alignment program with a PAM120 scoring matrix, a gap length penalty of 12, and a gap penalty of 4.

~~Figure 10 comprises Figures 10A through 10G. The nucleotide sequence (SEQ ID NO: 71) of a cDNA encoding the human TANGO 229 protein described herein is listed in Figures 10A through 10F. The open reading frame (ORF; residues 72 to 2216; SEQ ID NO: 72) of the cDNA is indicated by nucleotide triplets, above which the amino acid sequence (SEQ ID NO: 73) of human TANGO 229 is listed.~~ Figure 7[[10G]] is a hydrophobicity plot of one embodiment of human TANGO 229 protein.

~~Figure 11 comprises Figures 11A through 11Z-6.~~

~~The nucleotide sequence (SEQ ID NO: 81) of a cDNA encoding form 1a of the human INTERCEPT 289 protein described herein is listed in Figures 11A through 11C. The ORF (residues 179 to 742; SEQ ID NO: 82) of the cDNA is indicated by nucleotide triplets, above which the amino acid sequence (SEQ ID NO: 83) of form 1a of human INTERCEPT 289 is listed.~~

~~The nucleotide sequence (SEQ ID NO: 91) of a cDNA encoding form 1b of human INTERCEPT 289 protein described herein is listed in Figures 11D through 11G. The ORF (residues 179 to 712; SEQ ID NO: 92) of the cDNA is indicated by nucleotide triplets, above which the amino acid sequence (SEQ ID NO: 93) of form 1b of human INTERCEPT 289 is listed.~~

~~The nucleotide sequence (SEQ ID NO: 96) of a cDNA encoding form 2a of human INTERCEPT 289 protein described herein is listed in Figures 11H through 11K. The ORF (residues 162 to 656; SEQ ID NO: 97) of the cDNA is indicated by nucleotide triplets, above which the amino acid sequence (SEQ ID NO: 98) of form 2a of human INTERCEPT 289 is listed.~~

~~The nucleotide sequence (SEQ ID NO: 101) of a cDNA encoding form 2b of human INTERCEPT 289 protein described herein is listed in Figures 11L through 11O. The ORF (residues 162 to 626; SEQ ID NO: 102) of the cDNA is indicated by nucleotide triplets, above which the amino acid sequence (SEQ ID NO: 103) of form 2b of human INTERCEPT 289 is listed.~~

~~The nucleotide sequence (SEQ ID NO: 106) of a cDNA encoding form 3a of human INTERCEPT 289 protein described herein is listed in Figures 11P through 11S. The ORF (residues 162 to 596; SEQ ID NO: 107) of the cDNA is indicated by nucleotide triplets, above which the amino acid sequence (SEQ ID NO: 108) of form 3a of human INTERCEPT 289 is listed.~~

~~The nucleotide sequence (SEQ ID NO: 111) of a cDNA encoding form 3b of human INTERCEPT 289 protein described herein is listed in Figures 11T through 11V. The ORF (residues 162 to 566; SEQ ID NO: 112) of the cDNA is indicated by nucleotide triplets, above which the amino acid sequence (SEQ ID NO: 113) of form 3b of human INTERCEPT 289 is listed.~~

Figure 8[[11W]] is an alignment, made using the Wisconsin™ BestFit software (Smith and Waterman, (1981) Adv. Appl. Math. 2:482-489; BLOSUM62 scoring matrix, gap opening penalty 10 /

gap extension penalty 10) of the amino acid sequences of murine myeloid DNAX accessory protein associated lectin-1 ("M"; MDL-1; SEQ ID NO: 88), murine INTERCEPT 289 ("R"; SEQ ID NO: 163), human MDL-1 ("H"; SEQ ID NO: 86), form 1a of INTERCEPT 289 ("A"; SEQ ID NO: 83), form 1b of INTERCEPT 289 ("B"; SEQ ID NO: 93), form 2a of INTERCEPT 289 ("C"; SEQ ID NO: 98), form 2b of INTERCEPT 289 ("D"; SEQ ID NO: 103), form 3a of INTERCEPT 289 ("E"; SEQ ID NO: 108), and form 3b of INTERCEPT 289 ("F"; SEQ ID NO: 113).

Figures 9A-9N~~11X-6 through 11X-14~~ is an alignment (made using the Wisconsin™ BestFit software; Smith and Waterman, (1981) Adv. Appl. Math. 2:482-489; gap opening penalty 10 / gap extension penalty 10), of the nucleotide sequences of cDNA molecules encoding form 1a of INTERCEPT 289 ("A"; SEQ ID NO: 81), form 1b of INTERCEPT 289 ("B"; SEQ ID NO: 91), form 2a of INTERCEPT 289 ("C"; SEQ ID NO: 96), form 2b of INTERCEPT 289 ("D"; SEQ ID NO: 101), form 3a of INTERCEPT 289 ("E"; SEQ ID NO: 106), and form 3b of INTERCEPT 289 ("F"; SEQ ID NO: 111).

Figures 10A-10F~~11Y-1 through 11Y-6~~ is a series of hydrophobicity plots for individual forms of human INTERCEPT 289 protein. The plot corresponding to form 1a is shown in Figure 10A~~11Y-1~~. The plot corresponding to form 1b is shown in Figure 10B~~11Y-2~~. The plot corresponding to form 2a is shown in Figure 10C~~11Y-3~~. The plot corresponding to form 2b is shown in Figure 10D~~11Y-4~~. The plot corresponding to form 3a is shown in Figure 10E~~11Y-5~~. The plot corresponding to form 3b is shown in Figure 10F~~11Y-6~~.

~~The nucleotide sequence (SEQ ID NO: 161) of a cDNA encoding murine INTERCEPT 289 protein described herein is listed in Figures 11Z-1 through 11Z-3. The ORF (residues 198 to 767; SEQ ID NO: 162) of the cDNA is indicated by nucleotide triplets, beneath which the amino acid sequence (SEQ ID NO: 163) of murine INTERCEPT 289 is listed.~~ Figures 11A-11B~~11Z-4 and 11Z-5~~ are a manual alignment of the nucleotide sequences of murine INTERCEPT 289 ORF ("MI289"; SEQ ID NO: 162) and the ORF of form 1a of human INTERCEPT 289 ("HI289"; SEQ ID NO: 82). Figure 12~~11Z-6~~ is a hydrophobicity plot for murine INTERCEPT 289 protein.

~~Figure 12 comprises Figures 12A through 12T. The nucleotide sequence (SEQ ID NO: 121) of a cDNA encoding the human INTERCEPT 309 protein described herein is listed in Figures 12A through 12C. The ORF (residues 2 to 646; SEQ ID NO: 122) of the cDNA is indicated by nucleotide triplets, above which the amino acid sequence (SEQ ID NO: 123) of human INTERCEPT 309 is listed.~~ Figure 13[[12D]] is a hydrophobicity plot of human INTERCEPT 309 protein. An alignment (made using the ALIGN software; pam120.mat scoring matrix, gap opening penalty = 12, gap extension penalty = 4) of the nucleotide sequences of a cDNA clone ("DKFZ"; SEQ ID NO: 134; GenBank accession no. AL049977) obtained from human fetal brain tissue and INTERCEPT 309 cDNA ("I309"; SEQ ID NO: 121) is shown in Figures 14A-14G~~12E through 12K~~. An alignment (made using the

ALIGN software; pam120.mat scoring matrix, gap opening penalty = 12, gap extension penalty = 4) of the nucleotide sequences of the cDNA encoding human INTERCEPT 309 ("I309"; SEQ ID NO: 121) and a portion of a cDNA encoding murine claudin-8 protein ("CLAUD8"; SEQ ID NO: 132) is shown in Figures 15A-15G~~12L through 12R~~. An alignment (made using the ALIGN software; pam120.mat scoring matrix, gap opening penalty = 12, gap extension penalty = 4) of the amino acid sequences of human INTERCEPT 309 protein ("I309"; SEQ ID NO: 123) and murine claudin-8 protein ("CLAUD8"; SEQ ID NO: 133) is shown in Figure 16[[12S]]. A manual alignment of individual alignments (made using the Wisconsin™ BestFit software; Smith and Waterman (1981) Adv. Appl. Math. 2:482-489; blosum62 scoring matrix, gap opening penalty 10 / gap extension penalty 10) of the amino acid sequences of human INTERCEPT 309 protein ("I309"; SEQ ID NO: 123) with each of human Clostridium perfringens enterotoxin receptor ("hCPE"; SEQ ID NO: 135), murine C. perfringens enterotoxin receptor ("mCPE"; SEQ ID NO: 136), and a protein encoded by a cDNA recovered from regressing rat ventral prostate tissue ("rRPV"; SEQ ID NO: 137) is shown in Figure 17[[12T]].

~~Figure 13 comprises Figures 13A and 13B. The nucleotide sequence (SEQ ID NO: 141) of a cDNA encoding the human MANGO 419 protein described herein is listed in Figure 13A. The ORF (residues 84 to 323; SEQ ID NO: 142) of the cDNA is indicated by nucleotide triplets, above which the amino acid sequence (SEQ ID NO: 143) of human MANGO 419 is listed.~~ Figure 18[[13B]] is a hydrophobicity plot of human MANGO 419 protein.

~~Figure 14 comprises Figures 14A and 14B. The nucleotide sequence (SEQ ID NO: 151) of a cDNA encoding the human INTERCEPT 429 protein described herein is listed in Figure 14A. The ORF (residues 95 to 439; SEQ ID NO: 152) of the cDNA is indicated by nucleotide triplets, above which the amino acid sequence (SEQ ID NO: 153) of human INTERCEPT 429 is listed.~~ Figure 19[[14B]] is a hydrophobicity plot of human INTERCEPT 429 protein.

~~Figure 15 comprises Figures 15A through 15Y. The nucleotide sequence (SEQ ID NO: 171) of a cDNA encoding the human TANGO 210 protein described herein is listed in Figures 15A, 15B, 15C, and 15D. The open reading frame (ORF; residues 45 to 1583; SEQ ID NO: 172) of the cDNA is indicated by nucleotide triplets, above which the amino acid sequence (SEQ ID NO: 173) of human TANGO 210 is listed.~~ Figure 20[[15E]] is a hydrophobicity plot of human TANGO 210 protein (the conformation of the alternative form of TANGO 210 protein, wherein the carboxyl terminal portion comprises a transmembrane domain, is shown here). ~~The nucleotide sequence (SEQ ID NO: 181) of a cDNA encoding the murine TANGO 210 protein described herein is listed in Figures 15F, 15G, 15H, and 15I. The ORF (residues 22 to 927 and 1280 to 1906; collectively, SEQ ID NO: 182) of the cDNA is indicated by nucleotide triplets, above which the amino acid sequence (SEQ ID NO: 183) of murine TANGO 210 is listed.~~ Figure 21[[15J]] is a hydrophobicity plot of murine TANGO 210 protein. An alignment of the

amino acid sequences of human TANGO 210 protein (SEQ ID NO: 173) and murine TANGO 210 protein (SEQ ID NO: 183) amino acid sequences is shown in Figures 22A-22B~~15K and 15L~~, wherein identical amino acid residues are indicated by ":" and similar amino acid residues are indicated by ".". An alignment of the nucleotide sequences of the human (SEQ ID NO: 171) and murine (SEQ ID NO: 181) cDNAs encoding TANGO 210 protein is shown in Figures 23A-23I~~15M through 15U~~. Figures 24A-24B~~15V and 15W~~ are an alignment of the amino acid sequences of human TANGO 210 protein ("210"; SEQ ID NO: 173) and human matrix metalloproteinase-8 (MMP-8; "MMP-8"; SEQ ID NO: 176). An alignment of the nucleotide sequences of the open reading frame (ORF) encoding human TANGO 210 ("210"; SEQ ID NO: 172) and the ORF encoding human MMP-8 (SEQ ID NO: 177) is shown in Figures 24A-25F~~15X-1 through 15X-6~~. Figure 26[[15Y]] is a graph which depicts expression of TANGO 210 mRNA in selected human tissue and cell types, relative to TANGO 210 expression in the human fetal heart tissue.

~~Figure 16 comprises Figures 16A through 16E. The nucleotide sequence (SEQ ID NO: 191) of a cDNA encoding the human TANGO 366 protein described herein is listed in Figures 16A through 16D. The ORF (residues 86 to 1144; SEQ ID NO: 192) of the cDNA is indicated by nucleotide triplets, above which the amino acid sequence (SEQ ID NO: 193) of human TANGO 366 is listed.~~ Figure 27[[16E]] is a hydrophobicity plot of human TANGO 366 protein.

~~Figure 17 comprises Figures 17A through 17M. The nucleotide sequence (SEQ ID NO: 201) of a cDNA encoding the human INTERCEPT 394 protein described herein is listed in Figures 17A through 17F. The ORF (residues 320 to 2653; SEQ ID NO: 202) of the cDNA is indicated by nucleotide triplets, above which the amino acid sequence (SEQ ID NO: 203) of human INTERCEPT 394 is listed.~~ Figure 28[[17G]] is a hydrophobicity plot of human INTERCEPT 394 protein. ~~The nucleotide sequence (SEQ ID NO: 201) of a cDNA encoding the human INTERCEPT 394 protein described herein is listed in Figures 17H through 17M. The alternative ORF (residues 120 to 2567; SEQ ID NO: 215) of the cDNA is indicated by nucleotide triplets, above which the amino acid sequence (SEQ ID NO: 216) of this alternative form of human INTERCEPT 394 protein is listed.~~

~~Figure 18 comprises Figures 18A through 18R. The nucleotide sequence (SEQ ID NO: 221) of a cDNA encoding the human INTERCEPT 400 protein described herein is listed in Figures 18A through 18C. The ORF (residues 206 to 1000; SEQ ID NO: 222) of the cDNA is indicated by nucleotide triplets, above which the amino acid sequence (SEQ ID NO: 223) of human INTERCEPT 400 is listed.~~ Figure 29[[18D]] is a hydrophobicity plot of human INTERCEPT 400 protein. ~~The nucleotide sequence (SEQ ID NO: 241) of a cDNA encoding the murine INTERCEPT 400 protein described herein is listed in Figures 18E and 18F. The ORF (residues 3 to 524; SEQ ID NO: 242) of the cDNA is indicated by nucleotide triplets, above which the amino acid sequence (SEQ ID NO: 243) of murine INTERCEPT 400 is listed.~~ Figure 30[[18G]] is a hydrophobicity plot of murine INTERCEPT 400 protein. An alignment of

the amino acid sequences of human INTERCEPT 400 protein (SEQ ID NO: 223) and murine INTERCEPT 400 protein (SEQ ID NO: 243) amino acid sequences is shown in Figure 31[[18H]]. An alignment of the nucleotide sequences of the human (SEQ ID NO: 222) and murine (SEQ ID NO: 242) ORFs encoding INTERCEPT 400 protein is shown in Figures 32A-32C~~18I through 18K~~. Figure 33[[18L]] is an alignment of the amino acid sequences of human INTERCEPT 400 protein ("I400"; SEQ ID NO: 223) and murine Cig30 protein ("CIG30"; SEQ ID NO: 239). An alignment of the nucleotide sequences of the ORFs encoding human INTERCEPT 400 protein ("I400"; SEQ ID NO: 222) and the ORF encoding murine Cig30 ("CIG30"; SEQ ID NO: 238) is shown in Figures 34A-34C~~18M through 18O~~. ~~The nucleotide sequence (SEQ ID NO: 251) of a cDNA encoding the rat INTERCEPT 400 protein described herein is listed in Figures 18P and 18Q. The ORF (residues 1 to 432; SEQ ID NO: 252) of the cDNA is indicated by nucleotide triplets, above which the amino acid sequence (SEQ ID NO: 253) of rat INTERCEPT 400 is listed.~~ Figure 35[[18R]] is an alignment of the amino acid sequences of human (SEQ ID NO: 223), murine (SEQ ID NO: 243), and rat (SEQ ID NO: 253) INTERCEPT 400 proteins.

~~Figure 19 comprises Figures 19A through 19M. The nucleotide sequence (SEQ ID NO: 271) of a cDNA encoding the human INTERCEPT 217 protein described herein is listed in Figures 19A through 19E. The open reading frame (ORF; residues 215 to 1579; SEQ ID NO: 272) of the cDNA is indicated by nucleotide triplets, above which the amino acid sequence (SEQ ID NO: 273) of human INTERCEPT 217 is listed.~~ Figure 36[[19F]] is a hydrophobicity plot of human INTERCEPT 217 protein. An alignment of the amino acid sequences of human INTERCEPT 217 protein ("H"; SEQ ID NO: 273) and porcine ribonuclease inhibitor protein ("P"; SwissProt Accession number P10775; SEQ ID NO: 334) is shown in Figures 37A-37B~~19G and 19H~~. These alignments were made using the ALIGN software {Myers and Miller (1989) CABIOS, ver. 2.0}; pam120.mat scoring matrix; gap opening penalty = 12, gap extension penalty = 4). ~~The nucleotide sequence (SEQ ID NO: 362) of an ORF encoding the murine INTERCEPT 217 protein described herein is listed in Figures 19I through 19K. The ORF (residues 1 to 960; SEQ ID NO: 362) is indicated by nucleotide triplets, beneath which the amino acid sequence (SEQ ID NO: 363) of murine INTERCEPT 217 is listed.~~ Figure 38[[19L]] is a hydrophobicity plot of murine INTERCEPT 217 protein. An alignment of the amino acid sequences of human INTERCEPT 217 protein ("H"; SEQ ID NO: 273) and murine INTERCEPT 217 protein ("M"; SEQ ID NO: 363) is shown in Figure 39[[1M]]. These alignments were made using the BESTFIT software (BLOSUM62 scoring matrix, gap opening penalty = 12, frameshift gap penalty = 5, gap extension penalty = 4).

~~Figure 20 comprises Figures 20A through 20D. The nucleotide sequence (SEQ ID NO: 279) of a cDNA encoding the human INTERCEPT 297 protein described herein is listed in Figures 20A, 20B, and 20C. The open reading frame (ORF; residues 40 to 1152; SEQ ID NO: 280) of the cDNA is indicated by nucleotide triplets, above which the amino acid sequence (SEQ ID NO: 281) of human INTERCEPT 297 is listed.~~ Figure 40[[20D]] is a hydrophobicity plot of human INTERCEPT 297 protein.

~~Figure 21 comprises Figures 21A through 21R. The nucleotide sequence (SEQ ID NO: 303) of a cDNA encoding the human TANGO 276 protein described herein is listed in Figures 21A to 21D. The ORF (residues 58 to 786; SEQ ID NO: 304) of the cDNA is indicated by nucleotide triplets, above which the amino acid sequence (SEQ ID NO: 305) of human TANGO 276 is listed.~~ Figure 41[[21E]] is a hydrophobicity plot of TANGO 276 protein. An alignment of the amino acid sequences of human TANGO 276 protein ("H"; SEQ ID NO: 305) and murine protein M-Sema-F ("M"; SEQ ID NO: 335) is shown in Figures 42A-42C~~21F to 21H~~. In Figures 43A-43J~~21I through 21R~~, an alignment of the nucleotide sequences of the cDNA encoding human TANGO 276 protein ("H"; SEQ ID NO: 303) and the nucleotide sequences of the cDNA encoding murine protein M-Sema-F ("M"; SEQ ID NO: 66) is shown. These alignments were made using the ALIGN software {Myers and Miller (1989) CABIOS, ver. 2.0}; pam120.mat scoring matrix; gap opening penalty = 12, gap extension penalty = 4).

~~Figure 22 comprises Figures 22A through 22M. The nucleotide sequence (SEQ ID NO: 308) of a cDNA encoding the human TANGO 292 protein described herein is listed in Figures 22A to 22C. The ORF (residues 205 to 882; SEQ ID NO: 309) of the cDNA is indicated by nucleotide triplets, beneath which the amino acid sequence (SEQ ID NO: 310) of human TANGO 292 is listed.~~ Figure 44[[22D]] is a hydrophobicity plot of human TANGO 292 protein. ~~The nucleotide sequence (SEQ ID NO: 351) of a cDNA encoding the gerbil TANGO 292 protein described herein is listed in Figures 22E to 22H. The ORF (residues 89 to 763; SEQ ID NO: 352) of the cDNA is indicated by nucleotide triplets, below which the amino acid sequence (SEQ ID NO: 353) of gerbil TANGO 292 is listed.~~ Figures 45A-45C~~22I to 22K~~ are an alignment of the nucleotide sequences of the ORF encoding human TANGO 292 protein ("H"; SEQ ID NO: 308) and the nucleotide sequence of the ORF encoding gerbil TANGO 292 protein ("G"; SEQ ID NO: 351), made using the ALIGN software {Myers and Miller (1989) CABIOS, ver. 2.0}; pam120.mat scoring matrix; gap opening penalty = 12, gap extension penalty = 4). Figure 46[[22L]] is an alignment of the human (H) and gerbil (G) TANGO 292 amino acid sequences, made using the same software and parameters. Figure 47[[22M]] is a hydrophobicity plot of gerbil TANGO 292 protein.

~~Figure 23 comprises Figures 23A through 23J. The nucleotide sequence (SEQ ID NO: 324) of a cDNA encoding the human TANGO 331 protein described herein is listed in Figures 23A, 23B, and 23C. The ORF (residues 114 to 1172; SEQ ID NO: 325) of the cDNA is indicated by nucleotide triplets, above which the amino acid sequence (SEQ ID NO: 326) of human TANGO 331 is listed.~~ Figure 48[[23D]] is a hydrophobicity plot of TANGO 331 protein. An alignment of the amino acid sequences of human TANGO 331 protein ("H"; SEQ ID NO: 326) and Chinese hamster protein HT ("C"; SEQ ID NO: 339; GenBank Accession No. U48852) is shown in Figure 49[[23E]]. In Figures 50A-50E~~23F through 23J~~, an alignment of the nucleotide sequences of the cDNA encoding human TANGO 331 protein ("H"; SEQ ID NO: 324) and the nucleotide sequence of the cDNA encoding Chinese hamster protein HT ("C"; SEQ ID

NO: 340) is shown. These alignments were made using the ALIGN software {Myers and Miller (1989) CABIOS, ver. 2.0}; pam120.mat scoring matrix; gap opening penalty = 12, gap extension penalty = 4).

~~Figure 24 comprises Figures 24A through 24U. The nucleotide sequence (SEQ ID NO: 329) of a cDNA encoding the human TANGO 332 protein described herein is listed in Figures 24A through 24E. The ORF (residues 173 to 2185; SEQ ID NO: 330) of the cDNA is indicated by nucleotide triplets, above which the amino acid sequence (SEQ ID NO: 331) of human TANGO 332 protein is listed.~~ Figure 51[[24F]] is a hydrophobicity plot of TANGO 332 protein. An alignment of the amino acid sequences of TANGO 332 protein ("332"; SEQ ID NO: 331) and BEF protein ("BEF"; SEQ ID NO: 341) is shown in Figures 52A-52B~~24G and 24H~~. An alignment of the amino acid sequences of human TANGO 332 protein ("H"; SEQ ID NO: 331) and murine brevidin protein ("M"; SEQ ID NO: 342) is shown in Figures 53A-53C~~24I to 24K~~. In Figures 54A-54J~~24L through 24U~~, an alignment of the nucleotide sequences of the cDNA encoding human TANGO 332 protein ("H"; SEQ ID NO: 330) and the nucleotide sequence of the cDNA encoding murine brevidin protein ("M"; SEQ ID NO: 343) is shown. These alignments were made using the ALIGN software {Myers and Miller (1989) CABIOS, ver. 2.0}; pam120.mat scoring matrix; gap opening penalty = 12, gap extension penalty = 4).

~~Figure 25 comprises Figures 25A to 25M. The nucleotide sequence (SEQ ID NO: 371) of a cDNA encoding the human TANGO 202 protein described herein is listed in Figures 25A to 25D. The open reading frame (ORF; residues 34 to 1458; SEQ ID NO: 372) of the cDNA is indicated by nucleotide triplets, above which the amino acid sequence (SEQ ID NO: 373) of human TANGO 202 is listed. The nucleotide sequence (SEQ ID NO: 437) of a cDNA encoding the murine TANGO 202 protein described herein is listed in Figures 25E to 25I. The ORF (residues 81 to 1490; SEQ ID NO: 438) of the cDNA is indicated by nucleotide triplets, above which the amino acid sequence (SEQ ID NO: 439) of murine TANGO 202 is listed.~~ An alignment of the amino acid sequences of human ("Hum."; SEQ ID NO: 373) and murine ("Mur."; SEQ ID NO: 439) TANGO 202 protein is shown in Figures 55A-55B~~25J and 25K~~. Figure 56A[[25L]] is a hydrophobicity plot of human TANGO 202 protein. Figure 56B[[25M]] is a hydrophobicity plot of murine TANGO 202 protein.

~~Figure 26 comprises Figures 26A to 26Q-19. The nucleotide sequence (SEQ ID NO: 379) of a cDNA encoding the human TANGO 234 protein described herein is listed in Figures 26A to 26I. The ORF (residues 28 to 4386; SEQ ID NO: 380) of the cDNA is indicated by nucleotide triplets, above which the amino acid sequence (SEQ ID NO: 381) of human TANGO 234 is listed.~~ Figure 57[[26J]] is a hydrophobicity plot of human TANGO 234 protein. An alignment of the amino acid sequences of human TANGO 234 ("Hum"; SEQ ID NO: 381) and bovine WC1 ("WC1"; SEQ ID NO: 448) proteins is shown in Figures 58A-58F~~26K to 26P~~. An alignment of the nucleotide sequences of an ORF encoding human TANGO 234 ("Hum"; SEQ ID NO: 380) and an ORF encoding bovine WC1 ("WC1"; SEQ ID NO: 449) proteins is shown in Figures 59A-59Q~~26Q-1 to 26Q-19~~.

~~Figure 27 comprises Figures 27A to 27U. The nucleotide sequence (SEQ ID NO: 387) of a cDNA encoding the human TANGO 265 protein described herein is listed in Figures 27A to 27E. The ORF (residues 32 to 2314; SEQ ID NO: 388) of the cDNA is indicated by nucleotide triplets, above which the amino acid sequence (SEQ ID NO: 389) of human TANGO 265 is listed.~~ An alignment of the amino acid sequences of human TANGO 265 protein ("Hum."; SEQ ID NO: 389) and murine semaphorin B protein ("Mur."; SEQ ID NO: 440; GenBank Accession No. X85991) is shown in Figures 60A-60C~~27F to 27H~~. In Figures 61A-61L~~27I to 27T~~, an alignment of the nucleotide sequences of the cDNA encoding human TANGO 265 protein ("Hum."; SEQ ID NO: 387) and the nucleotide sequences of the cDNA encoding murine semaphorin B protein ("Mur."; SEQ ID NO: 441; GenBank Accession No. X85991) is shown. Figure 62[[27U]] is a hydrophobicity plot of TANGO 265 protein.

~~Figure 28 comprises Figures 28A to 28I. The nucleotide sequence (SEQ ID NO: 403) of a cDNA encoding the human TANGO 286 protein described herein is listed in Figures 28A to 28D. The ORF (residues 133 to 1497; SEQ ID NO: 404) of the cDNA is indicated by nucleotide triplets, above which the amino acid sequence (SEQ ID NO: 405) of human TANGO 286 is listed.~~ Figure 63[[28E]] is a hydrophobicity plot of TANGO 286 protein. An alignment of the amino acid sequences of human TANGO 286 ("286"; SEQ ID NO: 405) and BPI protein ("BPI"; SEQ ID NO: 408) protein is shown in Figures 64A-64B~~28F and 28G~~. An alignment of the amino acid sequences of human TANGO 286 ("286"; SEQ ID NO: 405) and RENP protein ("RENP"; SEQ ID NO: 409) is shown in Figures 65A-65B~~28H and 28I~~.

~~Figure 29 comprises Figures 29A to 29H. The nucleotide sequence (SEQ ID NO: 415) of a cDNA encoding the human TANGO 294 protein described herein is listed in Figures 29A to 29C. The ORF (residues 126 to 1394; SEQ ID NO: 416) of the cDNA is indicated by nucleotide triplets, above which the amino acid sequence (SEQ ID NO: 417) of human TANGO 294 is listed.~~ An alignment of the amino acid sequences of human TANGO 294 protein ("294"; SEQ ID NO: 417) and a known human lipase protein ("HLP"; SEQ ID NO: 445; GenBank Accession No. NP_004181) is shown in Figures 66A-66B~~29D and 29E~~. Figure 67[[29F]] is a hydrophobicity plot of TANGO 294 protein. An alignment of the amino acid sequences of human TANGO 294 protein ("294"; SEQ ID NO: 417) and a known human lysosomal acid lipase protein ("LAL"; SEQ ID NO: 411) is shown in Figures 68A-68B~~29G and 29H~~.

~~Figure 30 comprises Figures 30A to 30G. The nucleotide sequence (SEQ ID NO: 423) of a cDNA encoding the human INTERCEPT 296 protein described herein is listed in Figures 30A to 30C. The ORF (residues 70 to 1098; SEQ ID NO: 424) of the cDNA is indicated by nucleotide triplets, above which the amino acid sequence (SEQ ID NO: 425) of human INTERCEPT 296 protein is listed.~~ Figure 69[[30D]] is a hydrophobicity plot of INTERCEPT 296 protein. An alignment of the amino acid sequences of human INTERCEPT 296 protein ("296"; SEQ ID NO: 425) and C. elegans C06E1.3 related protein ("CRP"; SEQ ID NO: 410) is shown in Figures 70A-70B~~30E through 30G~~.

Please amend the paragraph beginning on line 14 of page 36 as follows:

The full length of a cDNA which was isolated from a human fetal spleen cDNA library and which encodes human TANGO 416 protein (~~Figure 1;~~ SEQ ID NO: 1; i.e. the longer form of TANGO 416) is 5121 nucleotide residues. The open reading frame (ORF) of this cDNA, nucleotide residues 376 to 3780 of SEQ ID NO: 1 (i.e., SEQ ID NO: 2), encodes a 1135-amino acid residue protein (~~Figure 1;~~ SEQ ID NO: 3), corresponding to a 1108-residue transmembrane mature protein.

Please amend the paragraph beginning on line 20 of page 43 as follows:

Figure 1[[3]] depicts a hydrophobicity plot of human TANGO 416 protein. Relatively hydrophobic regions are above the dashed horizontal line, and relatively hydrophilic regions are below the dashed horizontal line. The hydrophobic region which corresponds to amino acid residues 1 to 27 of SEQ ID NOs: 3 and 33 is the signal sequence of human TANGO 416 (SEQ ID NO: 4). As described elsewhere herein, relatively hydrophilic regions are generally located at or near the surface of a protein, and are more frequently effective immunogenic epitopes than are relatively hydrophobic regions. For example, the region of human TANGO 416 protein from about amino acid residue 450 to about amino acid residue 470 appears to be located at or near the surface of the protein, while the region from about amino acid residue 335 to about amino acid residue 345 appears not to be located at or near the surface.

Please amend the paragraph beginning on line 20 of page 44 as follows:

Residues 1651-4000 of SEQ ID NO: 1 (the nucleotide sequence of TANGO 416 cDNA) were aligned (using the ALIGN software with gap length penalty of 12, and a gap penalty of 4) with the nucleotide sequence of the human testis cDNA clone DKFZp434B0923 listed in GenBank accession number AL137471. This alignment, shown in Figures 2A-2H[[4]], was generated using the ALIGN software (using the BLOSUM62 scoring matrix, a gap opening penalty of 12, a gap extension penalty of 4, and a frameshift gap penalty of 5), and indicated 98.6% identity between the two sequences in the 2350-residue overlapping portion. The nucleotide sequence (SEQ ID NO: 2) of the ORF encoding TANGO 416 was aligned using the ALIGN software (with gap length penalty of 12, and a gap penalty of 4)) with the nucleotide sequence of the ORF of a murine protocadherin (GenBank™ accession number Y08715; Telo et al., 1998, J. Biol. Chem. 273:17565-17572), as shown in Figures 3A-3O[[5]]. This alignment was generated using the ALIGN software (using the BLOSUM62 scoring matrix, a gap opening penalty of 12, a gap extension penalty of 4, and a frameshift gap penalty of 5), and indicated 55.4% identity between the two sequences in the overlapping portion. Alignment of the amino acid sequence of TANGO 416 with the amino acid sequence of the murine protocadherin, as shown in Figures 4A-4E[[6]], indicated 32.8% sequence identity and 42.2 % sequence similarity. This alignment was

generated using the ALIGN software (using the BLOSUM62 scoring matrix, a gap opening penalty of 12, a gap extension penalty of 4).

Please amend the paragraph beginning on line 14 of page 54 as follows:

Homology of TANGO 416 protein with murine vascular endothelial cadherin-2 (mVE-cad-2; Telo et al., 1998, J. Biol. Chem. 273:17565-17572; GenBank™ accession number Y08715; sometimes designated protocadherin; see Figures 3A-3O[[5]] and 4A-4E[[6]]) is an indication that TANGO 416 is a human orthologue of that mVE-cad-2, and exhibits one or more of the same activities. That is, TANGO 416 can be involved in adherens junction formation and maintenance, and can thereby modulate endothelial permeability to plasma proteins and circulating cells.

Please amend the paragraph beginning on line 25 of page 56 as follows:

A cDNA encoding human TANGO 457 was identified by analyzing the sequences of clones present in a human uterine smooth muscle library for sequences that encode wholly secreted or transmembrane proteins. This analysis led to the identification of a clone, jthUa027h12, encoding human TANGO 457. The human TANGO 457 cDNA of this clone is 2330 nucleotides long (~~Figure 7;~~ SEQ ID NO: 51). The open reading frame of TANGO 457 comprises nucleotides 149 to 1243 of SEQ ID NO: 51 (SEQ ID NO: 52), and encodes a transmembrane protein comprising the 365 amino acid sequence depicted in ~~Figure 7 (~~SEQ ID NO: 53[[)]].

Please amend the paragraph beginning on line 1 of page 58 as follows:

Figure 5[[8]] depicts a hydrophobicity plot of the human TANGO 457 amino acid sequence shown in SEQ ID NO:53~~Figure 7~~. Relatively hydrophobic regions of the protein are shown above the horizontal line, and relatively hydrophilic regions of the protein are below the horizontal line. The cysteine residues (cys) and N-glycosylation site are indicated by short vertical lines just below the hydrophobicity trace.

Please amend the paragraph beginning on line 16 of page 59 as follows:

Figures 6A-6D [[9]] depict[[s]] a local alignment of the nucleic acid of human TANGO 457 shown in SEQ ID NO: 51 and a portion of the nucleotide sequence of human chromosome 11p14.3 PAC clone pDJ239b22, from nucleic acids 121077 to 122478 (SEQ ID NO: 61; AC003969). The alignment shows that there is a 100% nucleotide sequence identity between the TANGO 457 sequence of SEQ ID NO: 51 and human chromosome 11p14.3 PAC clone pDJ239b22, over the specified region. Genes known to map to the p14 region of human chromosome 11 include those encoding fetal brain protein 239

and hepatitis B virus integration site-1 ~~(see http://www.ncbi.nlm.nih.gov/htbin-post/Omim/getmap?d3076)~~.

Please amend the paragraph beginning on line 23 of page 67 as follows:

The full length of the cDNA encoding human TANGO 229 protein (~~Figure 10;~~ SEQ ID NO: 71) is 3594 nucleotide residues. The open reading frame (ORF) of this cDNA, nucleotide residues 72 to 2216 of SEQ ID NO: 71 (i.e., SEQ ID NO: 72), encodes a 715-amino acid residue protein (~~Figure 10;~~ SEQ ID NO: 73), corresponding to a 681-residue transmembrane mature protein.

Please amend the last two rows in Table II on page 71 as follows:

CUB domain	41 to 147	~~See Fig. 10~~
Factor V/VIII discoidin domain	258 to 409	~~See Fig. 10~~

Please amend the paragraph beginning on line 3 of page 74 as follows:

Figure 7[[10G]] depicts a hydrophobicity plot of human TANGO 229 protein. Relatively hydrophobic regions are above the dashed horizontal line, and relatively hydrophilic regions are below the dashed horizontal line. The hydrophobic region which corresponds to amino acid residues 1 to 34 of SEQ ID NO: 73 is the signal sequence of human TANGO 229 (SEQ ID NO: 74). As described elsewhere herein, relatively hydrophilic regions are generally located at or near the surface of a protein, and are more frequently effective immunogenic epitopes than are relatively hydrophobic regions. For example, the region of human TANGO 229 protein from about amino acid residue 50 to about amino acid residue 70 appears to be located at or near the surface of the protein, while the region from about amino acid residue 195 to about amino acid residue 210 appears not to be located at or near the surface.

Please amend the paragraphs beginning on line 18 of page 80 as follows:

1a) The full length of the cDNA encoding INTERCEPT 289 protein form 1a (~~Figures 11A-11C and~~ SEQ ID NO: 81) is 4074 nucleotide residues. The ORF of this cDNA, nucleotide residues 179 to 742 of SEQ ID NO: 81 (i.e., SEQ ID NO: 82), encodes a 188-amino acid residue protein having the amino acid sequence SEQ ID NO: 83.

1b) The full length of the cDNA encoding INTERCEPT 289 protein form 1b (~~Figures 11D-11G and~~ SEQ ID NO: 91) is 4018 nucleotide residues. The ORF of this cDNA, nucleotide residues 179 to 712 of SEQ ID NO: 91 (i.e., SEQ ID NO: 92), encodes a 178-amino acid residue protein having the amino acid sequence SEQ ID NO: 93.

2a) The full length of the cDNA encoding INTERCEPT 289 protein form 2a (~~Figures 11H-11K and~~ SEQ ID NO: 96) is 3985 nucleotide residues. The ORF of this cDNA, nucleotide

residues 162 to 656 of SEQ ID NO: 96 (i.e., SEQ ID NO: 97), encodes a 165-amino acid residue protein having the amino acid sequence SEQ ID NO: 98.

2b) The full length of the cDNA encoding INTERCEPT 289 protein form 2b (~~Figures 11L-11O and~~ SEQ ID NO: 101) is 3958 nucleotide residues. The ORF of this cDNA, nucleotide residues 162 to 626 of SEQ ID NO: 101 (i.e., SEQ ID NO: 102), encodes a 155-amino acid residue protein having the amino acid sequence SEQ ID NO: 103.

3a) The full length of the cDNA encoding INTERCEPT 289 protein form 3a (~~Figures 11P-11S and~~ SEQ ID NO: 106) is 3925 nucleotide residues. The ORF of this cDNA, nucleotide residues 162 to 596 of SEQ ID NO: 106 (i.e., SEQ ID NO: 107), encodes a 145-amino acid residue protein having the amino acid sequence SEQ ID NO: 108.

3b) The full length of the cDNA encoding INTERCEPT 289 protein form 3b (~~Figures 11T-11V and~~ SEQ ID NO: 111) is 3898 nucleotide residues. The ORF of this cDNA, nucleotide residues 162 to 566 of SEQ ID NO: 111 (i.e., SEQ ID NO: 112), encodes a 135-amino acid residue protein having the amino acid sequence SEQ ID NO: 113.

Please amend the paragraphs beginning on line 8 of page 83 as follows:

INTERCEPT 289 proteins and nucleic acid molecules encoding them comprise a family of molecules having certain conserved structural and functional features, as illustrated in Figures 8 and 9A-9N~~Figures 11W and 11X-1 through 11X-14~~.

In Figure 8[[11W]], the amino acid sequences of various forms of INTERCEPT 289 ("A"-"F"; SEQ ID NOs: 83, 93, 98, 103, 108, and 113) are shown, as aligned using the Wisconsin™ BestFit software (Smith and Waterman, (1981) Adv. Appl. Math. 2:482-489; blosum62 scoring matrix; gap opening penalty 10 / gap extension penalty 10). In Figures 9A-9N~~11X-1 through 11X-14~~, the nucleotide sequences (SEQ ID NOs: 81, 91, 96, 101, 106, and 111) of cDNA molecules encoding the six forms of INTERCEPT 289 protein described herein are aligned using the Wisconsin™ BestFit software (Smith and Waterman, (1981) Adv. Appl. Math. 2:482-489; gap opening penalty 10 / gap extension penalty 10). As indicated in these figures, the various forms of INTERCEPT 289 protein differ in the length of the polypeptide sequence between the transmembrane domain and the lectin C-type domain described below and in the amino acid sequence of the carboxyl-terminal portion of the protein.

Please amend Table IVA on page 84 as follows:

Table IVA

Type of Potential Modification Site or Domain	Amino Acid Residues of SEQ ID NO: ## (INTERCEPT 289 form)						Amino Acid Sequence
	83 (1a)	93 (1b)	98 (2a)	103 (2b)	108 (3a)	113 (3b)	
N-glycosylation site	32-35	32-35	32-35	32-35			NKSN
	93-96	93-96	70-73	70-73	50-53	50-53	NESR
	144-147	144-147	121-124	121-124	101-104	101-104	NNSV
	151-154		128-131		108-111		NVTN
Protein kinase C phosphorylation site	40-42	40-42	40-42	40-42			TTR
	63-65	63-65					TTR
	178-180		155-157		135-137		SYR
Casein kinase II phosphorylation site	86-89	86-89	63-66	63-66	43-46	43-46	STSE
	91-94	91-94	68-71	68-71	48-51	48-51	SWNE
	122-125	122-125	99-102	99-102	79-82	79-82	TDAE
		168-171		145-148		125-128	TKPE
N-myristoylation site	103-108	103-108	80-85	80-85	60-65	60-65	GSTLAI
	150-155		127-132		107-112		GNVTNQ
	165-170		142-147		122-127		GLTKTF
Lectin C-type domain	97-183	97-170	74-160	74-147	54-140	54-127	~~See Fig. 11~~

Please amend Table IVB on page 86 as follows:

Table IVB

Type of Potential Modification Site or Domain	Amino Acid Residues of SEQ ID NO: 163	Amino Acid Sequence
N-glycosylation site	51 to 54	NVSQ
	146 to 149	NNSV
	153 to 156	NVTN
Protein kinase C phosphorylation site	180 to 182	SYR
Casein kinase II phosphorylation site	88 to 91	SFSE
	155 to 158	TNQD
N-myristoylation site	105 to 110	GSTLAI
	152 to 157	GNVTNQ
	167 to 172	GLTKTY

Lectin C-type domain	99 to 185	~~See Fig. 11~~

Please amend the paragraphs beginning on line 6 of page 86 as follows:

INTERCEPT 289 proteins and cDNAs exhibit homology with human myeloid DAP12 (DNAX accessory protein, 12 kilodalton) associated lectin-1 (MDL-1), which is described in PCT Publication No. WO 99/06557, which is also incorporated herein by reference. In Figure 8[[11W]], the amino acid sequences of various forms of INTERCEPT 289 ("A"-"F" and "R"; SEQ ID NOs: 83, 93, 98, 103, 108, 113, and 163, respectively), human MDL-1 ("H"; SEQ ID NO: 86), and murine MDL-1 ("M"; SEQ ID NO: 88) proteins are shown, as aligned using the Wisconsin™ BestFit software (Smith and Waterman, (1981) Adv. Appl. Math. 2:482-489; BLOSUM62 scoring matrix; gap opening penalty 10 / gap extension penalty 10). Each of the seven forms of INTERCEPT 289 protein described herein has a lysine residue (i.e., at residue 116 of SEQ ID NOs: 83 and 93, at residue 93 of SEQ ID NOs: 98 and 103, at residue 73 of SEQ ID NOs: 108 and 113, and at residue 118 of SEQ ID NO: 163) that is not present in the described sequence (SEQ ID NO: 86) of human MDL-1 protein.

In the alignment shown in Figure 8[[11W]], the amino acid sequence (SEQ ID NO: 83) of form 1a of INTERCEPT 289 protein is 100% identical to that of human MDL-1 over the 187-amino acid residue overlapping region and about 72.7% identical to that of murine MDL-1 in the 165-amino acid residue overlapping region.

In the alignment shown in Figure 8[[11W]], the amino acid sequence (SEQ ID NO: 93) of form 1b of INTERCEPT 289 protein is about 85.9% identical to that of human MDL-1 over the 177-amino acid residue overlapping region and about 60.0% identical to that of murine MDL-1 in the 155-amino acid residue overlapping region.

In the alignment shown in Figure 8[[11W]], the amino acid sequence (SEQ ID NO: 98) of form 2a of INTERCEPT 289 protein is 100% identical to that of human MDL-1 over the 164-amino acid residue overlapping region and about 71.5% identical to that of murine MDL-1 in the 165-amino acid residue overlapping region.

In the alignment shown in Figure 8[[11W]], the amino acid sequence (SEQ ID NO: 103) of form 2b of INTERCEPT 289 protein is about 83.8% identical to that of human MDL-1 over the 154-amino acid residue overlapping region and about 58.7% identical to that of murine MDL-1 in the 155-amino acid residue overlapping region.

In the alignment shown in Figure 8[[11W]], the amino acid sequence (SEQ ID NO: 108) of form 3a of INTERCEPT 289 protein is about 83.3% identical to that of human MDL-1 over the 144-amino acid residue overlapping region and about 74.5% identical to that of murine MDL-1 in the 145-amino acid residue overlapping region.

In the alignment shown in Figure 8[[11W]], the amino acid sequence (SEQ ID NO: 113) of form 3b of INTERCEPT 289 protein is about 63.4% identical to that of human MDL-1 over the 134-amino acid residue overlapping region and about 60.0% identical to that of murine MDL-1 in the 135-amino acid residue overlapping region.

In the alignment shown in Figure 8[[11W]], the amino acid sequence (SEQ ID NO: 163) of murine INTERCEPT 289 protein is 100% identical to that of murine MDL-1 over the 190-amino acid residue overlapping region and about 85.7% identical to that of human MDL-1 in the 188-amino acid residue overlapping region.

In the alignment shown in Figures 11A-B~~11Z-5~~, the nucleotide sequence (SEQ ID NO: 162) of the ORF of murine INTERCEPT 289 is about 71.8% identical to that of the ORF of human INTERCEPT 289 form 1a.

Please amend the paragraph beginning on line 10 of page 89 as follows:

Figures 10A-10F~~11Y-1 through 11Y-6~~ depict hydrophobicity plots of the six forms of human INTERCEPT 289 protein described herein. Form 1a corresponds to Figure 10A~~11Y-1~~, and has the amino acid sequence SEQ ID NO: 83. Form 1b corresponds to Figure 10B~~11Y-2~~, and has the amino acid sequence SEQ ID NO: 93. Form 2a corresponds to Figure 10C~~11Y-3~~, and has the amino acid sequence SEQ ID NO: 98. Form 2b corresponds to Figure 10D~~11Y-4~~, and has the amino acid sequence SEQ ID NO: 103. Form 3a corresponds to Figure 10E~~11Y-5~~, and has the amino acid sequence SEQ ID NO: 108. Form 3b corresponds to Figure 10F~~11Y-6~~, and has the amino acid sequence SEQ ID NO: 113. Relatively hydrophobic regions are above the dashed horizontal line, and relatively hydrophilic regions are below the dashed horizontal line. As described elsewhere herein, relatively hydrophilic regions are generally located at or near the surface of a protein, and are more frequently effective immunogenic epitopes than are relatively hydrophobic regions. Figure 12~~11Z-6~~ depicts a hydrophobicity plot of the murine INTERCEPT 289 protein described herein.

Please amend the paragraph beginning on line 7 of page 92 as follows:

The full length of the cDNA encoding human INTERCEPT 309 protein (~~Figure 12;~~ SEQ ID NO: 121) is 1909 nucleotide residues. The ORF of this cDNA, nucleotide residues 2 to 646 of SEQ ID NO: 121 (i.e., SEQ ID NO: 122), encodes an approximately 215-amino acid residue integral membrane protein (~~Figure 12;~~ SEQ ID NO: 123) having three transmembrane regions in its mature (181-amino acid residue; SEQ ID NO: 138) form.

Please amend the paragraph beginning on line 6 of page 94 as follows:

Figure 13[[12D]] depicts a hydrophobicity plot of an embodiment of human INTERCEPT 309 protein. Relatively hydrophobic regions are above the dashed horizontal line, and relatively hydrophilic regions are below the dashed horizontal line. The hydrophobic regions which corresponds to about amino acid residues 72 to 92, 108 to 131, and 154 to 178 of SEQ ID NO: 123 are the transmembrane domains of human INTERCEPT 309 described above. As described elsewhere herein, relatively hydrophilic regions are generally located at or near the surface of a protein, and are more frequently effective immunogenic epitopes than are relatively hydrophobic regions. For example, the region of human INTERCEPT 309 protein from about amino acid residue 90 to about amino acid residue 100 appears to be located at or near the surface of the protein, while the region from about amino acid residue 70 to about amino acid residue 85 appears not to be located at or near the surface.

Please amend the paragraphs beginning on line 9 of page 95 as follows:

INTERCEPT 309 protein exhibits amino acid sequence homology with murine claudin-8 protein, as indicated in the alignment (made using the ALIGN software {Myers and Miller (1989) CABIOS, ver. 2.0}; pam120.mat scoring matrix; gap opening penalty = 12, gap extension penalty = 4) of the amino acid sequences of INTERCEPT 309 (SEQ ID NO: 123) and murine claudin-8 (SEQ ID NO: 132) proteins shown in Figure 16[[12S]]. In this alignment, the two amino acid sequences are about 80.0% identical. Furthermore, INTERCEPT 309 cDNA (SEQ ID NO: 121) is about 83.1% identical to the nucleotide sequence of cDNA encoding murine claudin-8 (SEQ ID NO: 133; GenBank accession no. AF087826) over the 639-residue overlapping region, as indicated in the alignment (made using the ALIGN software; pam120.mat scoring matrix; gap opening penalty = 12, gap extension penalty = 4) shown in Figures 15A-15G~~12L through 12R~~.

An alignment (made using the ALIGN software; pam120.mat scoring matrix; gap opening penalty = 12, gap extension penalty = 4) of the nucleotide sequences of a cDNA clone (SEQ ID NO: 134; GenBank accession no. AL049977) obtained from human fetal brain tissue and INTERCEPT 309 cDNA (SEQ ID NO: 121) is shown in Figures 14A-14G~~12E through 12K~~ and indicates 100% sequence identity between the sequences in the overlapping portion. The overlapping portion does not overlap the INTERCEPT 309 ORF, with the exception of nucleotide residues 1 and 28-32. It is recognized that 'overlap' of the human fetal brain cDNA clone sequence with these ORF residues is an artifact of the ALIGN software, and does not represent meaningful homology between residues 1 and 28-32 of the INTERCEPT 309 ORF and the corresponding residues of the human fetal brain cDNA clone. Nonetheless, isolation of this cDNA clone from fetal brain tissue is an indication that INTERCEPT 309 protein is expressed in fetal brain tissue.

Please amend the paragraph beginning on line 28 of page 96 as follows:

Individual alignments (made using the Wisconsin™ BestFit software; Smith and Waterman (1981) Adv. Appl. Math. 2:482-489; blosum62 scoring matrix, gap opening penalty 10 / gap extension penalty 10) of the amino acid sequence (SEQ ID NO: 123) of INTERCEPT 309 with the amino acid sequences of human (SEQ ID NO: 135; GenBank Accession No. 4502877) and murine (SEQ ID NO: 136; GenBank Accession No. BAA22985) receptors of Clostridium perfringens enterotoxin (CPE) and with the amino acid sequence (SEQ ID NO: 137) encoded by rat ventral prostate tissue during androgen withdrawal-induced tissue regression were manually aligned (by inserting a 'blank' at position 1 of the rRPV nucleotide sequence). The manually aligned alignments are shown in Figure 17[[12T]]. The amino acid sequence of INTERCEPT 309 protein is about 43% identical to the human CPE receptor amino acid sequence, about 45% identical to the murine CPE receptor amino acid sequence, and about 43% identical to the amino acid sequence encoded by the transcript obtained from regressing rat ventral prostate tissue.

Please amend the paragraph beginning on line 4 of page 98 as follows:

As indicated by its similarity to murine claudin-8 (e.g., as shown in Figure 16[[12S]]), INTERCEPT 309 is a claudin-like protein, and can exhibit one or more of the activities exhibited by murine claudin-8 and other claudins. Claudins are proteins that are involved in formation, maintenance, and regulation of tight junctions, which are intercellular junctions that occur between cells of tissues (e.g., epithelia and endothelia) having selective permeability (Morita et al. (1999) Proc. Natl. Acad. Sci. USA 96:511-516). Tight junctions can be associated with actin fibrils, and claudins can mediate interactions between actin fibrils and other components of the tight junction. Tissues in which tight junctions occur between adjacent cells can form sheets or other structures which exhibit selective trans-tissue permeability and in which the membrane and membrane-bound components of tissue-spanning cells can be selectively localized to one side (e.g., apical or basolateral side) of the tissue. By way of example, epithelial and endothelial tissues of kidney, liver, lung, and thyroid form barriers which permit transepithelial / transendothelial passage of certain compounds and cells (e.g., secreted / excreted products and immune system cells), but not others. Tight junction alterations have also been associated with tumor differentiation, particularly in thyroid tumors (Kerjaschki et al. (1979) Am. J. Pathol. 96:207-225; Cochand-Priollet et al. (1998) Ultrastruct. Pathol. 22:413-420). INTERCEPT 309 can have a role in each of these functions, both in normal tissue and in aberrant tissue (e.g., tissue of a patient afflicted with a disorder that affects the tissue).

Please amend the paragraph beginning on line 27 of page 99 as follows:

INTERCEPT 309, being a cell surface claudin-like protein, can be a substrate for interaction of pathogens (e.g., bacteria, toxins, and viruses) with host cells, and can mediate interaction of pathogens

with cells which express INTERCEPT 309. For example, Morita et al. (supra) determined that a murine claudin is a receptor for Clostridium perfringens enterotoxin (CPE). Similarity between the amino acid sequences of murine claudin-8 and INTERCEPT 309 indicates that INTERCEPT 309 can act as a receptor for CPE. Furthermore, amino acid sequence similarity between INTERCEPT 309 and other human and murine CPE receptors (e.g., GenBank Accession Nos. 4502877 and BAA22985, as indicated in Figure 17[[12T]]) is a further indication that INTERCEPT 309 can mediate interaction of CPE with cells upon which CPE acts. INTERCEPT 309 proteins, nucleic acids encoding them, and agents that modulate activity or expression of either of these can be used to prognosticate, diagnose, and treat disorders mediated by C. perfringens. Such disorders include, by way of example, gastrointestinal disorders (e.g., diarrhea, gastroenteritis, and other disorders associated with food poisoning, and certain types of pseudomembranous colitis), disorders associated with wound healing (e.g., gangrene), and other pathogenic infections (e.g., sepsis with or without intravascular hemolysis). INTERCEPT 309 can, of course, also mediate interaction of other pathogens with cells which express it.

Please amend the paragraph beginning on line 8 of page 104 as follows:

In addition to its structural and functional similarity with claudin proteins, INTERCEPT 309 protein is also similar in sequence to at least one protein regulator of apoptosis. As shown in Figure 17[[12T]], the amino acid sequence of INTERCEPT 309 is similar to the amino acid sequence of a protein (rRPV) which is expressed specifically in regressing rat ventral prostate tissue and epididymis. As described by Briehl et al. (1991, Mol. Endocrinol. 5:1381-1388), expression of this rat protein is elevated 3- to 8-fold in ventral prostate tissue upon induction of tissue regression mediated by withdrawal of androgens. Androgen withdrawal induces apoptosis in rat ventral prostate tissue. Thus, the rat protein described by Briehl et al. (supra) is an apoptosis-associated protein. INTERCEPT 309, having a sequence similar to that of rRPV, can also modulate apoptosis in tissues in which it is expressed.

Please amend the paragraph beginning on line 19 of page 105 as follows:

The full length of the cDNA encoding human MANGO 419 protein (~~Figure 13;~~ SEQ ID NO: 141) is 323 nucleotide residues. The ORF of this cDNA, nucleotide residues 84 to 323 of SEQ ID NO: 141 (i.e., SEQ ID NO: 142), encodes an 80-amino acid residue (or longer) protein (~~Figure 13;~~ SEQ ID NO: 143), corresponding to a 56-residue (or longer) secreted mature protein.

Please amend the paragraph beginning on line 11 of page 107 as follows:

Figure 18[[13B]] depicts a hydrophobicity plot of human MANGO 419 protein. Relatively hydrophobic regions are above the dashed horizontal line, and relatively hydrophilic regions are below

the dashed horizontal line. The hydrophobic region which corresponds to amino acid residues 1 to about 24 of SEQ ID NO: 143 is the signal sequence of human MANGO 419 (SEQ ID NO: 144). As described elsewhere herein, relatively hydrophilic regions are generally located at or near the surface of a protein, and are more frequently effective immunogenic epitopes than are relatively hydrophobic regions. For example, the region of human MANGO 419 protein from about amino acid residue 35 to about amino acid residue 55 appears to be located at or near the surface of the protein, while the region from about amino acid residue 60 to about amino acid residue 65 appears not to be located at or near the surface.

Please amend the paragraph beginning on line 15 of page 112 as follows:

The full length of the cDNA encoding human INTERCEPT 429 protein (~~Figure 14;~~ SEQ ID NO: 151) is 546 nucleotide residues. The ORF of this cDNA, nucleotide residues 95 to 439 of SEQ ID NO: 151 (i.e., SEQ ID NO: 152), encodes a 115-amino acid residue protein (~~Figure 14;~~ SEQ ID NO: 153), corresponding to a 93-residue transmembrane mature protein.

Please amend the paragraph beginning on line 10 of page 114 as follows:

Figure 19[[14B]] depicts a hydrophobicity plot of human INTERCEPT 429 protein. Relatively hydrophobic regions are above the dashed horizontal line, and relatively hydrophilic regions are below the dashed horizontal line. The hydrophobic region which corresponds to amino acid residues 1 to 22 of SEQ ID NO: 153 is the signal sequence of human INTERCEPT 429 (SEQ ID NO: 154). As described elsewhere herein, relatively hydrophilic regions are generally located at or near the surface of a protein, and are more frequently effective immunogenic epitopes than are relatively hydrophobic regions. For example, the region of human INTERCEPT 429 protein from about amino acid residue 85 to about amino acid residue 100 appears to be located at or near the surface of the protein.

Please amend the paragraph beginning on line 1 of page 117 as follows:

The full length of the cDNA encoding human TANGO 210 protein (~~Figure 15;~~ SEQ ID NO: 171) is 1684 nucleotide residues. The open reading frame (ORF) of this cDNA, nucleotide residues 45 to 1583 of SEQ ID NO: 171 (i.e., SEQ ID NO: 172), encodes a 513-amino acid residue protein (~~Figure 15;~~ SEQ ID NO: 173), corresponding to a 496-residue secreted protein.

Please amend the last two rows of Table IX on page 119 and the first two rows of Table IX on page 120 as follows:

Hemopexin domain signature	318 to 333	~~See Fig. 15~~
Hemopexin domain	285 to 327 329 to 371 376 to 423 425 to 465	~~See Fig. 15~~
Peptidase_M10 domain	36 to 202	~~See Fig. 15~~
Neutral zinc metallopeptidase zinc-binding domain signature	213 to 222	~~See Fig. 15~~

Please amend the second to fifth row of Table X on page 121 as follows:

Hemopexin domain signature	319 to 334	~~See Fig. 15~~
Hemopexin domain	286 to 328 330 to 372 377 to 424 426 to 466	~~See Fig. 15~~
Zinc-binding metallopeptidase_M10 domain	36 to 202	~~See Fig. 15~~
Neutral zinc metallopeptidase zinc-binding domain signature	214 to 223	~~See Fig. 15~~

Please amend the paragraph beginning on line 28 of page 123 as follows:

Figure 20[[15E]] depicts a hydrophobicity plot of human TANGO 210 protein. Relatively hydrophobic regions are above the dashed horizontal line, and relatively hydrophilic regions are below the dashed horizontal line. The hydrophobic region which corresponds to amino acid residues 1 to about 17 of SEQ ID NO: 173 is the signal sequence of human TANGO 210 (SEQ ID NO: 174). The hydrophobic region which corresponds to amino acid residues 489 to 506 of SEQ ID NO: 173 is the transmembrane portion in the alternative form of human TANGO 210 protein. As described elsewhere herein, relatively hydrophilic regions are generally located at or near the surface of a protein, and are more frequently effective immunogenic epitopes than are relatively hydrophobic regions. For example, the region of human TANGO 210 protein from about amino acid residue 190 to about amino acid residue

205 appears to be located at or near the surface of the protein, while the region from about amino acid residue 145 to about amino acid residue 155 appears not to be located at or near the surface.

Please amend the paragraphs beginning on line 3 of page 125 as follows:

Human TANGO 210 exhibits sequence similarity to human MMP-8 (GENBANK™ Accession No. J05556), as indicated herein in Figures 24A-24B~~15V and 15W~~, which list an alignment of the amino acid sequences of these proteins. Figures 25A-25F~~15X-1 through 15X-6~~ depict an alignment of the nucleotide sequences of the ORFs of human TANGO 210 (SEQ ID NO: 172) and MMP-8 (SEQ ID NO: 176). In these alignments (each made using the ALIGN software; pam120.mat scoring matrix; gap penalties -12/-4), the amino acid and ORF nucleotide sequences corresponding to these two proteins are 43.9% identical and 57.1% identical, respectively.

The full length of the cDNA encoding murine TANGO 210 protein (~~Figure 15;~~ SEQ ID NO: 181) is 2467 nucleotide residues. The ORF of this cDNA, nucleotide residues 22 to 927 and about 1280 to 1906 of SEQ ID NO: 181 (i.e., collectively, SEQ ID NO: 182), encodes a 510-amino acid residue protein (~~Figure 15;~~ SEQ ID NO: 183). It is recognized that the precise locations of the intron boundaries in SEQ ID NO: 181 have not been identified. Thus, murine TANGO 210 protein can comprise one or more additional or one or more fewer amino acid residues at the exon-exon boundary (i.e., between about residues 302 and 303 of SEQ ID NO: 183).

Please amend the paragraph beginning on line 9 of page 126 as follows:

Figure 21[[15J]] depicts a hydrophobicity plot of murine TANGO 210 protein. Relatively hydrophobic regions are above the dashed horizontal line, and relatively hydrophilic regions are below the dashed horizontal line. The hydrophobic region which corresponds to amino acid residues 1 to about 17 of SEQ ID NO: 183 is the signal sequence of murine TANGO 210 (SEQ ID NO: 184). As described elsewhere herein, relatively hydrophilic regions are generally located at or near the surface of a protein, and are more frequently effective immunogenic epitopes than are relatively hydrophobic regions. For example, the region of murine TANGO 210 protein from about amino acid residue 18 to about amino acid residue 28 appears to be located at or near the surface of the protein, while the region from about amino acid residue 148 to about amino acid residue 158 appears not to be located at or near the surface

Please amend the paragraph beginning on line 24 of page 126 as follows:

Human and murine TANGO 210 proteins exhibit considerable sequence similarity, as indicated herein in Figures 22A-22B~~15K and 15L~~. Figures 22A-22B~~15K and 15L~~ depict an alignment of human and murine TANGO 210 amino acid sequences (SEQ ID NOs: 173 and 183, respectively). In this alignment (made using the ALIGN software {Myers and Miller (1989) CABIOS, ver. 2.0}; pam120.mat

scoring matrix; gap penalties -12/-4), the proteins are 77.2% identical in the overlapping region (i.e., 393 identical residues out of 509 residues in the overlapping region, which includes amino acid residues 1-509 of SEQ ID NO: 173 and amino acid residues 1-509 of SEQ ID NO: 183). The human and murine cDNAs encoding TANGO 210 are 76.2% identical in the overlapping portions (i.e., nucleotide residues 29-1601 of SEQ ID NO: 171 and nucleotide residues 8-927 and 1280-1935 of SEQ ID NO: 181), as assessed using the same software and parameters and as indicated in Figures 23A-23I~~15M through 15U~~. In the respective ORFs, SEQ ID NOs: 171 and 181 are 81.7% identical.

Please amend the paragraph beginning on line 28 of page 128 as follows:

Figure 26[[15Y]] depicts expression of TANGO 210 in various tissues and cell lines as described above, relative to expression in fetal heart tissue. The results indicate significant expression in breast, skeletal muscle, colon, vein, aorta, testis, thyroid, and small intestine tissues.

Please amend the paragraph beginning on line 23 of page 135 as follows:

The full length of the cDNA encoding human TANGO 366 protein (~~Figure 16;~~ SEQ ID NO: 191) is 2628 nucleotide residues. The ORF of this cDNA, nucleotide residues 86 to 1144 of SEQ ID NO: 191 (i.e., SEQ ID NO: 192), encodes a 353-amino acid residue protein (~~Figure 16;~~ SEQ ID NO: 193), corresponding to a 337-residue transmembrane protein.

Please amend the last three rows of Table XII on page 138 as follows:

Leucine rich repeat amino terminal (LRRNT) domain	19 to 58	~~See Fig. 16~~
Leucine rich repeat (LRR) domain	59 to 82 85 to 108 109 to 132 133 to 155 185 to 206 207 to 229 230 to 254 255 to 279 280 to 303	~~See Fig. 16~~
Leucine zipper pattern	284 to 305	~~See Fig. 16~~

Please amend the paragraph beginning on line 7 of page 140 as follows:

Figure 27[[16E]] depicts a hydrophobicity plot of human TANGO 366 protein. Relatively hydrophobic regions are above the dashed horizontal line, and relatively hydrophilic regions are below the dashed horizontal line. The hydrophobic region which corresponds to amino acid residues 1 to about 16 of SEQ ID NO: 193 is the signal sequence of human TANGO 366 (SEQ ID NO: 194), and the hydrophobic region which corresponds to amino acid residues 217 to 239 of SEQ ID NO: 193 is the transmembrane region of TANGO 366 (SEQ ID NO: 197). As described elsewhere herein, relatively hydrophilic regions are generally located at or near the surface of a protein, and are more frequently effective immunogenic epitopes than are relatively hydrophobic regions. For example, the region of human TANGO 366 protein from about amino acid residue 315 to about amino acid residue 330 appears to be located at or near the surface of the protein, while the region from about amino acid residue 290 to about amino acid residue 305 appears not to be located at or near the surface.

Please amend the paragraph beginning on line 6 of page 143 as follows:

The full length of the cDNA encoding human INTERCEPT 394 protein (~~Figure 17;~~ SEQ ID NO: 201) is 3743 nucleotide residues. The ORF of this cDNA, nucleotide residues 320 to 2653 of SEQ ID NO: 201 (i.e., SEQ ID NO: 202), encodes a 778-amino acid residue protein (~~Figure 17;~~ SEQ ID NO: 203), corresponding to a 778-residue transmembrane protein. It is recognized that, in an alternative form, transcription of INTERCEPT 394 protein can be initiated at the ATG codon located at nucleotide residues 120-122 of SEQ ID NO 201. In this alternative form, INTERCEPT 394 protein has, at the amino-terminal end of SEQ ID NO: 203, an additional 61 amino acid residues, this additional portion having the amino acid sequence encoded by nucleotide residues 120-319 of SEQ ID NO: 201. ~~The sequences corresponding to the cDNA (SEQ ID NO: 217), ORF (SEQ ID NO: 215), and protein (SEQ ID NO: 216) of this alternate form are listed in Figures 17H through 17M.~~ In the following discussion, molecules of the two forms of INTERCEPT 394 are referred to individually and collectively as molecules of the corresponding type (e.g., cDNA or protein).

Please amend the paragraph beginning on line 16 of page 147 as follows:

Figure 28[[17G]] depicts a hydrophobicity plot of human INTERCEPT 394 protein. Relatively hydrophobic regions are above the dashed horizontal line, and relatively hydrophilic regions are below the dashed horizontal line. The hydrophobic region which corresponds to amino acid residues 1 to about 25 of SEQ ID NO: 203 is the signal sequence of human INTERCEPT 394 (SEQ ID NO: 204). Hydrophobic regions which corresponding to amino acid residues 71 to 87, 229 to 253, 320 to 336, and 346 to 364 of SEQ ID NO: 203 are the transmembrane regions of INTERCEPT 394 (SEQ ID NOs: 207, 209, 211, and 213, respectively). As described elsewhere herein, relatively hydrophilic regions are

generally located at or near the surface of a protein, and are more frequently effective immunogenic epitopes than are relatively hydrophobic regions. For example, the region of human INTERCEPT 394 protein from about amino acid residue 205 to about amino acid residue 225 appears to be located at or near the surface of the protein, while the region from about amino acid residue 410 to about amino acid residue 340 appears not to be located at or near the surface.

Please amend the paragraph beginning on line 18 of page 150 as follows:

The full length of the cDNA encoding human INTERCEPT 400 protein (~~Figure 18;~~ SEQ ID NO: 221) is 2989 nucleotide residues. The open reading frame (ORF) of this cDNA, nucleotide residues 206 to 1000 of SEQ ID NO: 221 (i.e., SEQ ID NO: 222), encodes a 265-amino acid residue immature protein (~~Figure 18;~~ SEQ ID NO: 223), corresponding to a 219-residue transmembrane protein.

Please amend the paragraph beginning on line 5 of page 155 as follows:

Figure 29[[18D]] depicts a hydrophobicity plot of human INTERCEPT 400 protein. Relatively hydrophobic regions are above the dashed horizontal line, and relatively hydrophilic regions are below the dashed horizontal line. The hydrophobic region which corresponds to amino acid residues 1 to about 46 of SEQ ID NO: 223 is the signal sequence of human INTERCEPT 400 (SEQ ID NO: 224). As described elsewhere herein, relatively hydrophilic regions are generally located at or near the surface of a protein, and are more frequently effective immunogenic epitopes than are relatively hydrophobic regions. For example, the region of human INTERCEPT 400 protein from about amino acid residue 218 to about amino acid residue 231 appears to be located at or near the surface of the protein, while the region from about amino acid residue 80 to about amino acid residue 95 appears not to be located at or near the surface.

Please amend the paragraphs beginning on line 21 of page 155 as follows:

Human INTERCEPT 400 exhibits sequence similarity to murine Cig30 protein (GENBANK™ Accession No. U97107), as indicated herein in Figure 33[[18L]], which lists an alignment (made using the ALIGN software; pam120.mat scoring matrix; gap penalties -12/-4) of the amino acid sequences of these proteins. Figures 34A-34C~~18M through 18O~~ depict an alignment (also made using the ALIGN software; pam120.mat scoring matrix; gap penalties -12/-4) of the nucleotide sequences of the ORFs of human INTERCEPT 400 (SEQ ID NO: 222) and Cig30 (SEQ ID NO: 238). In these alignments (made using the ALIGN software; pam120.mat scoring matrix, gap penalties -12/-4), the amino acid sequences of these two proteins are 43.3% identical and the ORF nucleotide sequences corresponding to these two proteins are 56.8% identical. The cDNAs corresponding to these two proteins were found to be 48.4% identical using the LALIGN software (pam120.mat scoring matrix; gap penalties -12/-4).

The length of the incomplete cDNA encoding the carboxyl-terminal portion of murine INTERCEPT 400 protein (~~Figure 18;~~ SEQ ID NO: 241) is 2032 nucleotide residues. The ORF of this cDNA, nucleotide residues 3 to 524 (SEQ ID NO: 242), encodes a protein comprising at least 180 amino acid residues (~~Figure 18;~~ SEQ ID NO: 243). It is recognized that murine INTERCEPT 400 protein has about 60-120, more likely 80-100, additional amino acid residues at the amino terminal end thereof.

Please amend the paragraph beginning on line 20 of page 156 as follows:

Figure 30[[18G]] depicts a hydrophobicity plot of murine INTERCEPT 400 protein. Relatively hydrophobic regions are above the dashed horizontal line, and relatively hydrophilic regions are below the dashed horizontal line. Hydrophobic regions corresponds to the identified transmembrane regions of murine INTERCEPT 400. As described elsewhere herein, relatively hydrophilic regions are generally located at or near the surface of a protein, and are more frequently effective immunogenic epitopes than are relatively hydrophobic regions. For example, the region from about amino acid residue 125 to about amino acid residue 140 appears to be located at or near the surface of the protein, while the region from about amino acid residue 14 to about amino acid residue 19 appears not to be located at or near the surface

Please amend the paragraphs beginning on line 3 of page 157 as follows:

Human and murine INTERCEPT 400 proteins exhibit considerable sequence similarity, as indicated herein in Figures 31 and 32A-32C~~18H through 18K~~. Figure 31[[18H]] depicts an alignment of human and murine INTERCEPT 400 amino acid sequences (SEQ ID NOs: 223 and 243, respectively). In this alignment (made using the ALIGN software; pam120.mat scoring matrix; gap penalties -12/-4), the proteins are 94.8% identical in the overlapping region (i.e., 163 identical residues out of 172 residues in the overlapping region, which includes amino acid residues 94-265 of SEQ ID NO: 223 and amino acid residues 1-174 of SEQ ID NO: 243). The human and murine ORFs encoding INTERCEPT 400 are 92.8% identical in the overlapping portions (i.e., nucleotide residues 280-795 of SEQ ID NO: 222 and nucleotide residues 1-522 of SEQ ID NO: 242), as assessed using the same software and parameters and as indicated in Figures 32A-32C~~18I through 18K~~ in an alignment made using the ALIGN software (pam120.mat scoring matrix; gap penalties -12/-4).

The partial nucleotide sequences of a rat cDNA clone (designated jtmba232b12; SEQ ID NO: 251) and ORF (SEQ ID NO: 252) encoding INTERCEPT 400 ~~are depicted in Figures 18P and 18Q, together with the amino acid sequence~~ (SEQ ID NO: 253) ~~of the portion of the protein encoded by these nucleic acids~~. An alignment (made using the ALIGN software; pam120.mat scoring matrix; gap penalties -12/-4) of human, murine and rat INTERCEPT 400 amino acid sequences is listed in Figure 35[[18R]].

Please amend the paragraph beginning on line 8 of page 160 as follows:

The full length of the cDNA encoding human INTERCEPT 217 protein (~~Figure 19;~~ SEQ ID NO: 271) is 2895 nucleotide residues. The ORF of this cDNA, nucleotide residues 215 to 1579 of SEQ ID NO: 271 (i.e., SEQ ID NO: 272), encodes a 455-amino acid transmembrane protein (~~Figure 19;~~ SEQ ID NO: 273). The murine ORF (~~Figure 19;~~ SEQ ID NO: 362) comprises at least 962 nucleotide residues. The protein encoded by the murine ORF comprises at least 320 amino acid residues (i.e., SEQ ID NO: 363), and is also a transmembrane protein.

Please amend the last four rows of Table XVIA on pages 163-164 as follows:

Leucine zipper pattern	45 to 66	~~See Fig. 19~~
Leucine rich repeat amino terminal domain (LLRNT)	33 to 61	~~See Fig. 19~~
Leucine rich repeat (LRR) Domain	62 to 85 86 to 109 110 to 133 134 to 157 158 to 181 184 to 207	~~See Fig. 19~~ ~~See Fig. 19~~ ~~See Fig. 19~~ ~~See Fig. 19~~ ~~See Fig. 19~~ ~~See Fig. 19~~
Leucine rich repeat carboxyl terminal (LLRCT) domain	219 to 274	~~See Fig. 19~~

Please amend the last three rows of Table XVIB on pages 165 as follows:

Immunoglobulin Domain	14 to 37	~~See Fig. 19~~
Leucine rich repeat (LRR) Domain	49 to 104	~~See Fig. 19~~
Leucine rich repeat carboxyl terminal (LLRCT) domain	123 to 184	~~See Fig. 19~~

Please amend the paragraph beginning on line 18 of page 168 as follows:

Human INTERCEPT 217 exhibits amino acid sequence similarity to porcine ribonuclease inhibitor, a protein which binds with high affinity to pancreatic ribonucleases and inhibits their activity. INTERCEPT 217 thus is involved with similar physiological processes in humans. An alignment of the amino acid sequences of human INTERCEPT 217 and porcine ribonuclease inhibitor protein (SwissProt Accession number P10775) is shown in Figure 37A[[19G]]. In this alignment (made using the ALIGN software {Myers and Miller (1989) CABIOS, ver. 2.0}; pam120.mat scoring matrix; gap opening penalty

= 12, gap extension penalty = 4), the proteins are 20.5% identical. An alignment of human (SEQ ID NO: 273) and murine INTERCEPT 217 amino acid sequences (SEQ ID NO: 363; made using BESTFIT software, BLOSUM62 scoring matrix, gap opening penalty = 12, frameshift gap penalty = 5, gap extension penalty = 4). In this alignment, the human and murine amino acid sequences are 71.3% identical in the overlapping region. Alignment of human and murine INTERCEPT 217 ORFs indicated 79.9% nucleotide sequence identity in the overlapping region.

Please amend the paragraph beginning on line 3 of page 170 as follows:

Figure 36[[19F]] depicts a hydrophobicity plot of human INTERCEPT 217 protein. Relatively hydrophobic regions are above the dashed horizontal line, and relatively hydrophilic regions are below the dashed horizontal line. The hydrophobic region which corresponds to amino acid residues 1 to 20 of SEQ ID NO: 273 is the signal sequence of human INTERCEPT 217 (SEQ ID NO: 274). The hydrophobic region which corresponds to amino acid residues 384 to 403 of SEQ ID NO: 273 is the transmembrane domain of human INTERCEPT 217 (SEQ ID NO: 277). As described elsewhere herein, relatively hydrophilic regions are generally located at or near the surface of a protein, and are more frequently effective immunogenic epitopes than are relatively hydrophobic regions. For example, the region of human INTERCEPT 217 protein from about amino acid residue 355 to about amino acid residue 380 appears to be located at or near the surface of the protein, while the region from about amino acid residue 190 to about amino acid residue 210 appears not to be located at or near the surface. Figure 38[[19L]] depicts a hydrophobicity plot of murine INTERCEPT 217 protein.

Please amend the paragraph beginning on line 6 of page 175 as follows:

The full length of the cDNA encoding human INTERCEPT 297 protein (~~Figure 20;~~ SEQ ID NO: 279) is 1518 nucleotide residues. The ORF of this cDNA, nucleotide residues 40 to 1152 of SEQ ID NO: 279 (i.e., SEQ ID NO: 280), encodes a 371-amino acid transmembrane protein (~~Figure 20;~~ SEQ ID NO: 281).

Please amend the last row of Table XVIII on page 178 as follows:

DUF6 domain	44 to 171	~~See Fig. 20~~

Please amend the paragraph beginning on line 18 of page 179 as follows:

Figure 40[[20D]] depicts a hydrophobicity plot of human INTERCEPT 297 protein. Relatively hydrophobic regions are above the dashed horizontal line, and relatively hydrophilic regions are below the dashed horizontal line. Hydrophobic region corresponding to the signal sequence and the transmembrane domains are observed in this figure. As described elsewhere herein, relatively

hydrophilic regions are generally located at or near the surface of a protein, and are more frequently effective immunogenic epitopes than are relatively hydrophobic regions. For example, the region of human INTERCEPT 297 protein from about amino acid residue 165 to about amino acid residue 175 appears to be located at or near the surface of the protein.

Please amend the paragraph beginning on line 24 of page 181 as follows:

The full length of the cDNA encoding human TANGO 276 protein (~~Figure 21;~~ SEQ ID NO: 303) is 2811 nucleotide residues. The ORF of this cDNA, nucleotide residues 58 to 786 of SEQ ID NO: 303 (i.e., SEQ ID NO: 304), encodes a 243-amino acid secreted protein (~~Figure 21;~~ SEQ ID NO: 305).

Please amend the paragraph beginning on line 23 of page 182 as follows:

TANGO 276 proteins and nucleic acid molecules encoding them comprise a family of molecules having certain conserved structural and functional features, as indicated by the conservation of amino acid sequence between human TANGO 276 protein and the murine protein designated M-Sema-F (see Inagaki et al. (1995) FEBS Lett. 370:269-272), as shown in Figures 42A-42C~~21F to 21H~~.

Please amend the last row of Table XIX on page 183 as follows:

Sema domain	53 to 141	~~See Fig. 21~~

Please amend the paragraph beginning on line 3 of page 184 as follows:

Human TANGO 276 protein exhibits considerable sequence similarity to murine M-Sema F protein (GenBank Accession no. S79463), as indicated herein in Figures 42A-42C~~21F to 21H~~. Figures 42A-42C~~21F to 21H~~ depict an alignment of the amino acid sequences of human TANGO 276 protein (SEQ ID NO: 305) and murine M-Sema F protein (SEQ ID NO: 335). In this alignment (pam120.mat scoring matrix, gap opening penalty = 12, gap extension penalty = 4), the amino acid sequences of the proteins are 76.1% identical. Figures 43A-43J~~21I through 21R~~ depict an alignment of the nucleotide sequences of cDNA encoding human TANGO 276 protein (SEQ ID NOs: 303) and murine cDNA encoding M-Sema F protein (SEQ ID NO: 336). In this alignment (pam120.mat scoring matrix, gap opening penalty = 12, gap extension penalty = 4), the nucleic acid sequences of the cDNAs are 79.7% identical. Thus, TANGO 276 is related to murine M-Sema F and shares functional similarities to that protein.

Please amend the paragraph beginning on line 28 of page 184 as follows:

Figure 41[[21E]] depicts a hydrophobicity plot of human TANGO 276 protein. Relatively hydrophobic regions are above the dashed horizontal line, and relatively hydrophilic regions are below

the dashed horizontal line. The hydrophobic region which corresponds to about amino acid residues 1 to 20 of SEQ ID NO: 305 is the signal sequence of human TANGO 276. As described elsewhere herein, relatively hydrophilic regions are generally located at or near the surface of a protein, and are more frequently effective immunogenic epitopes than are relatively hydrophobic regions. For example, the region of human TANGO 276 protein from about amino acid residue 90 to about amino acid residue 105 appears to be located at or near the surface of the protein, while the region from about amino acid residue 170 to about amino acid residue 180 appears not to be located at or near the surface.

Please amend the paragraph beginning on line 8 of page 189 as follows:

The full length of the cDNA encoding human TANGO 292 protein (~~Figure 22;~~ SEQ ID NO: 308) is 2498 nucleotide residues. The ORF of this cDNA, nucleotide residues 205 to 882 of SEQ ID NO: 308 (i.e., SEQ ID NO: 309), encodes a 226-amino acid residue transmembrane protein (~~Figure 22;~~ SEQ ID NO: 310). The full length of the cDNA encoding gerbil TANGO 292 protein (~~Figure 22;~~ SEQ ID NO: 351) is 2002 nucleotide residues. The ORF of this cDNA, nucleotide residues 89 to 763 of SEQ ID NO: 351 (i.e., SEQ ID NO: 352), encodes a 225-amino acid transmembrane protein (~~Figure 22;~~ SEQ ID NO: 353).

Please amend the last row of Table XXIa on page 191 as follows:

Vitamin K-dependent carboxylation domain	56 to 98	~~See Fig. 22~~

Please amend the last row of Table XXIb on page 192 as follows:

Vitamin K-dependent carboxylation domain	55 to 92	~~See Fig. 22~~

Please amend the paragraphs beginning on line 8 of page 195 as follows:

Figure 44[[22D]] depicts a hydrophobicity plot of human TANGO 292 protein. Relatively hydrophobic regions are above the dashed horizontal line, and relatively hydrophilic regions are below the dashed horizontal line. The hydrophobic region which corresponds to amino acid residues 1 to 17 of SEQ ID NO: 310 is the signal sequence of human TANGO 292. The hydrophobic region which corresponds to amino acid residues 114 to 138 of SEQ ID NO: 310 is the transmembrane domain of human TANGO 292. As described elsewhere herein, relatively hydrophilic regions are generally located at or near the surface of a protein, and are more frequently effective immunogenic epitopes than are relatively hydrophobic regions. For example, the region of human TANGO 292 protein from about amino acid residue 90 to about amino acid residue 110 appears to be located at or near the surface of the

protein, while the region from about amino acid residue 190 to about amino acid residue 195 appears not to be located at or near the surface.

Figure 47[[22M]] depicts a hydrophobicity plot of gerbil TANGO 292 protein. Relatively hydrophobic regions are above the dashed horizontal line, and relatively hydrophilic regions are below the dashed horizontal line. The hydrophobic region which corresponds to amino acid residues 1 to 17 of SEQ ID NO: 353 is the signal sequence of gerbil TANGO 292. The hydrophobic region which corresponds to amino acid residues 113 to 137 of SEQ ID NO: 353 is the transmembrane domain of gerbil TANGO 292. As described elsewhere herein, relatively hydrophilic regions are generally located at or near the surface of a protein, and are more frequently effective immunogenic epitopes than are relatively hydrophobic regions. For example, the region of gerbil TANGO 292 protein from about amino acid residue 90 to about amino acid residue 110 appears to be located at or near the surface of the protein.

An alignment of the human (H) and gerbil (G) ORF sequences encoding TANGO 292 protein is shown in Figures 45A-45C~~22I-22K~~. This alignment was made using the ALIGN software {Myers and Miller (1989) CABIOS, ver. 2.0}; pam120.mat scoring matrix; gap opening penalty = 12, gap extension penalty = 4), and indicates about 64.1% identity between these two cDNA sequences. An alignment of the amino acid sequences of gerbil (G) and human (H) TANGO 292 proteins is shown in Figure 46[[22L]]. In this alignment (made using the ALIGN software {Myers and Miller (1989) CABIOS, ver. 2.0}; pam120.mat scoring matrix; gap opening penalty = 12, gap extension penalty = 4), the proteins are about 77.7% identical and about 80% similar.

Please amend the paragraph beginning on line 19 of page 200 as follows:

The full length of the cDNA encoding human TANGO 331 protein (~~Figure 23;~~ SEQ ID NO: 324) is 1432 nucleotide residues. The ORF of this cDNA, nucleotide residues 114 to 1172 of SEQ ID NO: 324 (i.e., SEQ ID NO: 325), encodes a 353-amino acid secreted protein (~~Figure 23;~~ SEQ ID NO: 326).

Please amend the paragraph beginning on line 7 of page 201 as follows:

TANGO 331 proteins and nucleic acid molecules encoding them comprise a family of molecules having certain conserved structural and functional features, as indicated by the conservation of amino acid sequence between human TANGO 331 protein and the Chinese hamster (Cricetulus griseus) protein designated HT and having GenBank Accession number U48852, as shown in Figure 49[[23E]], and the conservation of nucleotide sequence between the ORFs encoding human TANGO 331 protein and Chinese hamster protein HT, as shown in Figures 50A-50E~~23F through 23J~~.

Please amend the last seven rows of Table XXII on page 203 as follows:

Aspartic acid and asparagine hydroxylation site	308 to 319	~~See Fig. 23~~
EGF-like domain cysteine pattern signature	166 to 177	~~See Fig. 23~~
EGF domain	140 to 177	~~See Fig. 23~~
	234 to 263	~~See Fig. 23~~
	301 to 330	~~See Fig. 23~~
Laminin-like EGF domain	153 to 199	~~See Fig. 23~~
TNFR/NGFR cysteine-rich region domain	180 to 214	~~See Fig. 23~~
Vertebrate metallothionein-like domain	229 to 298	~~See Fig. 23~~
Leucine Zipper domain	94 to 115	~~See Fig. 23~~

Please amend the paragraph beginning on line 8 of page 207 as follows:

TANGO 331 shares amino acid and nucleic acid homology with a Chinese hamster protein designated HT, and thus is involved in corresponding physiological processes in humans. An alignment of the amino acid sequences of (human) TANGO 331 and Chinese hamster protein HT is shown in Figure 49[[23E]]. In this alignment (made using the ALIGN software {Myers and Miller (1989) CABIOS, ver. 2.0}; pam120.mat scoring matrix; gap opening penalty = 12, gap extension penalty = 4), the proteins are 71.9% identical. An alignment of the nucleotide sequences of the ORFs encoding (human) TANGO 331 and Chinese hamster protein HT is shown in Figures 50A-50E~~23F through 23J~~. The two ORFs are 74.5% identical, as assessed using the same software and parameters.

Please amend the paragraph beginning on line 24 of page 207 as follows:

Figure 48[[23D]] depicts a hydrophobicity plot of human TANGO 331 protein. Relatively hydrophobic regions are above the dashed horizontal line, and relatively hydrophilic regions are below the dashed horizontal line. The hydrophobic region which corresponds to amino acid residues 1 to 24 of SEQ ID NO: 326 is the signal sequence of human TANGO 331 (SEQ ID NO: 327). As described elsewhere herein, relatively hydrophilic regions are generally located at or near the surface of a protein, and are more frequently effective immunogenic epitopes than are relatively hydrophobic regions. For example, the region of human TANGO 331 protein from about amino acid residue 140 to about amino acid residue 170 appears to be located at or near the surface of the protein, while the region from about amino acid residue 115 to about amino acid residue 130 appears not to be located at or near the surface.

Please amend the paragraph beginning on line 1 of page 214 as follows:

Mapping of the human TANGO 331 gene to chromosomal region 22q11-q13 is an indication of disorders with which its expression (or non- or aberrant-expression) can be associated. For example, arylsulfatase A is associated with Metachromatic leukodystrophy. Diaphorase (NADH:cytochrome b-5 reductase) is associated with methemoglobinemia, types I and II. Solute carrier family 5 (sodium/glucose transporter), member 1 is associated with glucose/galactose malabsorption. The gene designated schizophrenia 4 is associated with schizophrenia and velocardiofacial syndrome, as described in Online Mendelian Inheritance in Man, Johns Hopkins University, Baltimore, MD. MIM Number: 600850:12/7/98. ~~(World Wide Web URL: http://www.ncbi.nlm.nih.gov/omim/).~~ These mapping data indicate that TANGO 331 polypeptides, nucleic acids, and modulators thereof can be used to prognosticate, diagnose, inhibit, prevent, or alleviate one or more of these disorders.

Please amend the paragraph beginning on line 18 of page 214 as follows:

The full length of the cDNA encoding human TANGO 332 protein (~~Figure 24;~~ SEQ ID NO: 329) is 2730 nucleotide residues. The ORF of this cDNA, nucleotide residues 173 to 2185 of SEQ ID NO: 329 (i.e., SEQ ID NO: 330), encodes a 671-amino acid transmembrane protein (~~Figure 24;~~ SEQ ID NO: 331).

Please amend the paragraph beginning on line 7 of page 215 as follows:

TANGO 332 proteins and nucleic acid molecules encoding them comprise a family of molecules having certain conserved structural and functional features, as indicated by the conservation of amino acid sequence between human TANGO 332 protein, human brain-enriched hyaluronan-binding factor (BEF), as shown in Figures 52A-52B~~24G and 24H~~, and murine brevican protein, as shown in Figures 53A-53C~~24I to 24K~~. This conservation is further indicated by conservation of nucleotide sequence between the ORFs encoding human TANGO 332 protein and murine brevican protein, as shown in Figures 54A-54J~~24L through 24U~~.

Please amend the last two rows of Table XXIII on page 217 as follows:

Immunoglobulin-/major histocompatibility protein-like (Ig-/MHC-like) domain	50 to 141	~~See Fig. 24~~
Extracellular link domain	156 to 251 257 to 353	~~See Fig. 24~~ ~~See Fig. 24~~

Please amend the paragraphs beginning on line 1 of page 219 as follows:

An alignment of the amino acid sequences of TANGO 332 and BEF protein is shown in Figures 52A-52B~~24G and 24H~~. In this alignment (made using the ALIGN software {Myers and Miller (1989) CABIOS, ver. 2.0}; pam120.mat scoring matrix; gap opening penalty = 12, gap extension penalty = 4), the proteins are 75.7% identical, although it is seen that TANGO 332 includes two domains (one from about amino acid residue 152 to about residue 208, and the other near the carboxyl terminus of TANGO 332) which do not occur in BEF protein. It is likely that these two regions account for the differences between the physiological roles of TANGO 332 and BEF.

An alignment of the amino acid sequences of (human) TANGO 332 and murine brevican protein is shown in Figures 53A-53C~~24I through 24K~~. In this alignment (made using the ALIGN software {Myers and Miller (1989) CABIOS, ver. 2.0}; pam120.mat scoring matrix; gap opening penalty = 12, gap extension penalty = 4), the proteins are 75.5% identical, although it is seen that murine brevican protein includes a domain which does not occur in TANGO 332 protein, this domain is present from about amino acid residue 626 to the carboxyl terminus of murine brevican protein. An alignment of the nucleotide sequences of the ORFs encoding (human) TANGO 332 and murine brevican protein is shown in Figures 54A-54J~~24L through 24U~~. The two ORFs are 62.6% identical, as assessed using the same software and parameters.

Please amend the paragraph beginning on line 14 of page 220 as follows:

Figure 51[[24F]] depicts a hydrophobicity plot of human TANGO 332 protein. Relatively hydrophobic regions are above the dashed horizontal line, and relatively hydrophilic regions are below the dashed horizontal line. The hydrophobic region which corresponds to amino acid residues 1 to 22 of SEQ ID NO: 331 is the signal sequence of human TANGO 332 (SEQ ID NO: 332). As described elsewhere herein, relatively hydrophilic regions are generally located at or near the surface of a protein, and are more frequently effective immunogenic epitopes than are relatively hydrophobic regions. For example, the region of human TANGO 332 protein from about amino acid residue 445 to about amino acid residue 475 appears to be located at or near the surface of the protein, while the region from about amino acid residue 45 to about amino acid residue 62 appears not to be located at or near the surface.

Please amend the paragraph beginning on line 25 of page 222 as follows:

The full length of the cDNA encoding human TANGO 202 protein (~~Figure 25;~~ SEQ ID NO: 371) is 1656 nucleotide residues. The open reading frame (ORF) of this cDNA, nucleotide residues 34 to 1458 of SEQ ID NO: 371 (i.e., SEQ ID NO: 372), encodes a 475-amino acid transmembrane protein (~~Figure 25;~~ SEQ ID NO: 373).

Please amend the last two rows of Table XXIV on page 226 as follows:

Kringle Domain	34 to 116	~~See Fig. 25~~
CUB domain	216 to 320	~~See Fig. 25~~

Please amend the last two rows of Table XXV on page 228 as follows:

Kringle Domain	32 to 114	~~See Fig. 25~~
CUB domain	214 to 318	~~See Fig. 25~~

Please amend the paragraph beginning on line 12 of page 230 as follows:

Figure 56A[[25L]] depicts a hydrophobicity plot of human TANGO 202 protein. Relatively hydrophobic regions are above the dashed horizontal line, and relatively hydrophilic regions are below the dashed horizontal line. The hydrophobic region which corresponds to amino acid residues 1 to 19 of SEQ ID NO: 373 is the signal sequence of human TANGO 202 (SEQ ID NO: 374). The hydrophobic region which corresponds to amino acid residues 393 to 415 of SEQ ID NO: 373 is the transmembrane domain of human TANGO 202 (SEQ ID NO: 377). As described elsewhere herein, relatively hydrophilic regions are generally located at or near the surface of a protein, and are more frequently effective immunogenic epitopes than are relatively hydrophobic regions. For example, the region of human TANGO 202 protein from about amino acid residue 61 to about amino acid residue 95 appears to be located at or near the surface of the protein, while the region from about amino acid residue 395 to about amino acid residue 420 appears not to be located at or near the surface.

Please amend the paragraph beginning on line 3 of page 231 as follows:

The full length of the cDNA encoding murine TANGO 202 protein (~~Figure 25;~~ SEQ ID NO: 437) is 4928 nucleotide residues. The ORF of this cDNA, nucleotide residues 81 to 1490 of SEQ ID NO: 437 (i.e., SEQ ID NO: 438), encodes a 470-amino acid secreted protein (~~Figure 25;~~ SEQ ID NO: 439).

Please amend the paragraph beginning on line 12 of page 231 as follows:

Figure 56B[[25M]] depicts a hydrophobicity plot of murine TANGO 202 protein. Relatively hydrophobic regions are above the dashed horizontal line, and relatively hydrophilic regions are below the dashed horizontal line. The hydrophobic region which corresponds to amino acid residues 1 to 19 of SEQ ID NO: 439 is the signal sequence of murine TANGO 202 (SEQ ID NO: 412). As described elsewhere herein, relatively hydrophilic regions are generally located at or near the surface of a protein, and are more frequently effective immunogenic epitopes than are relatively hydrophobic regions. For example, the region of murine TANGO 202 protein from about amino acid residue 61 to about amino acid

residue 95 appears to be located at or near the surface of the protein, while the region from about amino acid residue 295 to about amino acid residue 305 appears not to be located at or near the surface

Please amend the paragraph beginning on line 27 of page 231 as follows:

Human and murine TANGO 202 proteins exhibit considerable sequence similarity, as indicated herein in Figures 55A-55B~~25J and 25K~~. Figures 55A-55B~~25J and 25K~~ depict an alignment of human and murine TANGO 202 amino acid sequences (SEQ ID NOs: 373 and 439, respectively). In this alignment (made using the ALIGN software {Myers and Miller (1989) CABIOS, ver. 2.0}; pam120.mát scoring matrix; gap penalties -12/-4), the proteins are 76.5% identical. The human and murine ORFs encoding TANGO 202 are 87.4% identical, as assessed using the same software and parameters.

Please amend the paragraph beginning on line 20 of page 235 as follows:

The full length of the cDNA encoding human TANGO 234 protein (~~Figure 26;~~ SEQ ID NO: 379) is 4628 nucleotide residues. The ORF of this cDNA, nucleotide residues 28 to 4386 of SEQ ID NO: 379 (i.e., SEQ ID NO: 380), encodes a 1453-amino acid transmembrane protein (~~Figure 26;~~ SEQ ID NO: 381).

Please amend the paragraph beginning on line 9 of page 236 as follows:

TANGO 234 proteins and nucleic acid molecules encoding them comprise a family of molecules having certain conserved structural and functional features, as indicated by the conservation of amino acid sequence between human TANGO 234 protein and bovine WC1 protein, as shown in Figures 58A-58F~~26K through 26P~~, and the conservation of nucleotide sequence between the ORFs encoding human TANGO 234 protein and bovine WC1 protein, as shown in Figures 59A-59Q~~26Q-1 through 26Q-19~~.

Please amend the last two rows of Table XXVII on page 242 as follows:

Speract receptor repeated (SRR) domain signature	53 to 90	~~See Fig. 26~~
	160 to 197	~~See Fig. 26~~
	267 to 304	~~See Fig. 26~~
	1041 to 1078	~~See Fig. 26~~
	1251 to 1288	~~See Fig. 26~~
Scavenger receptor cysteine-rich (SRCR) domain	51 to 148	~~See Fig. 26~~
	158 to 255	~~See Fig. 26~~
	265 to 362	~~See Fig. 26~~
	372 to 469	~~See Fig. 26~~

	479 to 576	~~See Fig. 26~~
	586 to 683	~~See Fig. 26~~
	693 to 790	~~See Fig. 26~~
	798 to 895	~~See Fig. 26~~
	903 to 1000	~~See Fig. 26~~
	1039 to 1136	~~See Fig. 26~~
	1146 to 1243	~~See Fig. 26~~
	1249 to 1346	~~See Fig. 26~~

Please amend the paragraph beginning on line 21 of page 244 as follows:

TANGO 234 is likely the human orthologue of ruminant protein WC1, and thus is involved with the physiological processes described above in humans. An alignment of the amino acid sequences of (human) TANGO 234 and bovine WC1 protein is shown in Figures 58A-58F~~26K-26P~~. In this alignment (made using the ALIGN software {Myers and Miller (1989) CABIOS, ver. 2.0}; pam120.mat scoring matrix; gap penalties -12/-4), the proteins are 40.4% identical. An alignment of the nucleotide sequences of the ORFs encoding (human) TANGO 234 and bovine WC1 protein is shown in Figures 59A-59Q~~26Q-1 to 26Q-19~~. The two ORFs are 54.3% identical, as assessed using the same software and parameters.

Please amend the paragraph beginning on line 12 of page 245 as follows:

Figure 57[[26J]] depicts a hydrophobicity plot of human TANGO 234 protein. Relatively hydrophobic regions are above the dashed horizontal line, and relatively hydrophilic regions are below the dashed horizontal line. The hydrophobic region which corresponds to amino acid residues 1 to 40 of SEQ ID NO: 381 is the signal sequence of human TANGO 234 (SEQ ID NO: 382). The hydrophobic region which corresponds to amino acid residues 1360 to 1383 of SEQ ID NO: 381 is the transmembrane domain of human TANGO 234 (SEQ ID NO: 385). As described elsewhere herein, relatively hydrophilic regions are generally located at or near the surface of a protein, and are more frequently effective immunogenic epitopes than are relatively hydrophobic regions. For example, the region of human TANGO 234 protein from about amino acid residue 225 to about amino acid residue 250 appears to be located at or near the surface of the protein, while the region from about amino acid residue 990 to about amino acid residue 1000 appears not to be located at or near the surface.

Please amend the paragraph beginning on line 14 of page 248 as follows:

The full length of the cDNA encoding human TANGO 265 protein (~~Figure 27;~~ SEQ ID NO: 387) is 3104 nucleotide residues. The ORF of this cDNA, nucleotide residues 32 to 2314 of SEQ ID NO: 387 (i.e., SEQ ID NO: 388), encodes a 761-amino acid transmembrane protein (~~Figure 27;~~ SEQ ID NO: 389).

Please amend the last row of Table XXIX on page 251 as follows:

Sema domain	64 to 478	~~See Fig. 27~~

Please amend the paragraph beginning on line 8 of page 252 as follows:

Human TANGO 265 protein exhibits considerable sequence similarity to murine semaphorin B protein (GenBank Accession no. X85991), as indicated herein in Figures 60A-60C~~27F to 27H~~. Figures 60A-60C~~27F to 27H~~ depict an alignment of the amino acid sequences of human TANGO 265 protein (SEQ ID NO: 389) and murine semaphorin B protein (SEQ ID NO: 446). In this alignment (pam120.mat scoring matrix, gap penalties -12/-4), the amino acid sequences of the proteins are 82.3% identical. Figures 61A-61L~~27I through 27T~~ depict an alignment of the nucleotide sequences of cDNA encoding human TANGO 265 protein (SEQ ID NO: 387) and murine cDNA encoding semaphorin B protein (SEQ ID NO: 447). In this alignment (pam120.mat scoring matrix, gap penalties -12/-4), the nucleic acid sequences of the cDNAs are 76.2% identical. Thus, TANGO 265 is the human orthologue of murine semaphorin B and shares functional similarities to that protein.

Please amend the paragraph beginning on line 7 of page 253 as follows:

Figure 62[[27U]] depicts a hydrophobicity plot of human TANGO 265 protein. Relatively hydrophobic regions are above the dashed horizontal line, and relatively hydrophilic regions are below the dashed horizontal line. The hydrophobic region which corresponds to amino acid residues 1 to 31 of SEQ ID NO: 389 is the signal sequence of human TANGO 265 (SEQ ID NO: 390). The hydrophobic region which corresponds to amino acid residues 684 to 704 of SEQ ID NO: 389 is the transmembrane domain of human TANGO 265 (SEQ ID NO: 393). As described elsewhere herein, relatively hydrophilic regions are generally located at or near the surface of a protein, and are more frequently effective immunogenic epitopes than are relatively hydrophobic regions. For example, the region of human TANGO 265 protein from about amino acid residue 350 to about amino acid residue 375 appears to be located at or near the surface of the protein, while the region from about amino acid residue 230 to about amino acid residue 250 appears not to be located at or near the surface.

Please amend the paragraph beginning on line 9 of page 255 as follows:

The full length of the cDNA encoding TANGO 286 protein (~~Figure 28;~~ SEQ ID NO: 403) is 1980 nucleotide residues. The ORF of this cDNA, nucleotide residues 133 to 1497 of SEQ ID NO: 403 (i.e., SEQ ID NO: 404), encodes a 455-amino acid secreted protein (~~Figure 28;~~ SEQ ID NO: 405).

Please amend the last row of Table XXX on page 257 as follows:

Lipid-binding serum glycoprotein domain	12 to 427	~~see Fig. 28~~

Please amend the paragraph beginning on line 16 of page 258 as follows:

Figure 63[[28E]] depicts a hydrophobicity plot of TANGO 286 protein. Relatively hydrophobic regions are above the dashed horizontal line, and relatively hydrophilic regions are below the dashed horizontal line. As described elsewhere herein, relatively hydrophilic regions are generally located at or near the surface of a protein, and are more frequently effective immunogenic epitopes than are relatively hydrophobic regions. For example, the region of human TANGO 286 protein from about amino acid residue 420 to about amino acid residue 435 appears to be located at or near the surface of the protein, while the region from about amino acid residue 325 to about amino acid residue 345 appears not to be located at or near the surface.

Please amend the paragraph beginning on line 11 of page 261 as follows:

The full length of the cDNA encoding TANGO 294 protein (~~Figure 29;~~ SEQ ID NO: 415) is 2044 nucleotide residues. The ORF of this cDNA, nucleotide residues 126 to 1394 of SEQ ID NO: 415 (i.e., SEQ ID NO: 416), encodes a 423-amino acid transmembrane protein (~~Figure 29;~~ SEQ ID NO: 417).

Please amend the last row of Table XXXI on page 263 as follows:

Alpha/beta hydrolase fold domain	125 to 404	~~See Fig. 29~~

Please amend the paragraph beginning on line 7 of page 264 as follows:

Figure 67[[29F]] depicts a hydrophobicity plot of human TANGO 294 protein. Relatively hydrophobic regions are above the dashed horizontal line, and relatively hydrophilic regions are below the dashed horizontal line. The hydrophobic region which corresponds to amino acid residues 1 to 33 of SEQ ID NO: 417 is the signal sequence of human TANGO 294 (SEQ ID NO: 419). The hydrophobic region which corresponds to amino acid residues 255 to 279 of SEQ ID NO: 417 is the predicted transmembrane domain of human TANGO 294 (SEQ ID NO: 421). As described elsewhere herein, relatively hydrophilic regions are generally located at or near the surface of a protein, and are more frequently effective immunogenic epitopes than are relatively hydrophobic regions. For example, the region of human TANGO 294 protein from about amino acid residue 130 to about amino acid residue 150 appears to be located at or near the surface of the protein, while the region from about amino acid residue 90 to about amino acid residue 100 appears not to be located at or near the surface.

Please amend the paragraph beginning on line 1 of page 265 as follows:

Human TANGO 294 protein exhibits considerable sequence similarity (i.e., about 75% amino acid sequence identity) to lingual and gastric lipase proteins of rat (Swissprot Accession no. P04634; Docherty et al. (1985) Nucleic Acids Res. 13:1891-1903), dog (Swissprot Accession no. P80035; Carriere et al. (1991) Eur. J. Biochem. 202:75-83), and human (Swissprot Accession no. P07098; Bernbaeck and Blaeckberg (1987) Biochim. Biophys. Acta 909:237-244), as assessed using the ALIGN v. 2.0 computer software using a pam12.mat scoring matrix and gap penalties of -12/-4. TANGO 294 is distinct from the known human lipase, as indicated in Figures 66A-66B~~29D and 29E~~. Figures 66A-66B~~29D and 29E~~ depict an alignment of the amino acid sequences of human TANGO 294 protein (SEQ ID NO: 417) and the known human lipase protein (SEQ ID NO: 445), as assessed using the same software and parameters. In this alignment (pam120.mat scoring matrix, gap penalties -12/-4), the amino acid sequences of the proteins are 49.8% identical. TANGO 294 also is distinct from the known human lysosomal acid lipase, as indicated in Figures 68A-68B~~29G and 29H~~. Figures 68A-68B~~29G and 29H~~ depicts an alignment of the amino acid sequences of human TANGO 294 protein (SEQ ID NO: 417) and the known human lysosomal acid lipase protein (SEQ ID NO: 411). In this alignment (pam120.mat scoring matrix, gap penalties -12/-4), the amino acid sequences of the proteins are 56.9% identical.

Please amend the paragraph beginning on line 3 of page 267 as follows:

The full length of the cDNA encoding INTERCEPT 296 protein (~~Figure 30;~~ SEQ ID NO: 423) is 2133 nucleotide residues. The ORF of this cDNA, nucleotide residues 70 to 1098 of SEQ ID NO: 423 (i.e., SEQ ID NO: 424), encodes a 343-amino acid transmembrane protein (~~Figure 30;~~ SEQ ID NO: 425).

Please amend the paragraph beginning on line 4 of page 269 as follows:

Figure 69[[30D]] depicts a hydrophobicity plot of INTERCEPT 296 protein. Relatively hydrophobic regions are above the dashed horizontal line, and relatively hydrophilic regions are below the dashed horizontal line. The hydrophobic regions which corresponds to amino acid residues 24 to 42, 51 to 70, 183 to 204, 211 to 227, and 250 to 271 of SEQ ID NO: 425 are the transmembrane domains of human INTERCEPT 296 (SEQ ID NOs: 429 through 433, respectively). As described elsewhere herein, relatively hydrophilic regions are generally located at or near the surface of a protein, and are more frequently effective immunogenic epitopes than are relatively hydrophobic regions. For example, the region of human INTERCEPT 296 protein from about amino acid residue 120 to about amino acid residue 140 appears to be located at or near the surface of the protein, while the region from about amino acid residue 95 to about amino acid residue 110 appears not to be located at or near the surface.

Please amend the paragraph beginning on line 19 of page 269 as follows:

Figures 70A-70B~~30E through 30G~~ depicts an alignment of the amino acid sequences of human INTERCEPT 296 protein (SEQ ID NO: 425) and Caenorhabditis elegans C06E1.3 related protein (SEQ ID NO: 410). In this alignment (pam120.mat scoring matrix, gap penalties -12/-4), the amino acid sequences of the proteins are 26.8% identical. The C. elegans protein has five predicted transmembrane domains.

Please amend Tables A-1, A-2 and A-3 on pages 271-272 as follows:

Table A-1

Protein Designation	SEQ ID NOs			~~Depicted in Figure #~~	ATCC® Accession #
	cDNA	ORF	Protein		
TANGO 416	1	2	3	~~1~~	PTA-1764
TANGO416 (alt.form)	32	32	33	~~1~~	PTA-1764
TANGO 457	51	52	53	~~7~~	PTA-817
TANGO 229	71	72	73	~~10~~	PTA-295
INTERCEPT 289					PTA-295
form 1a	81	82	83	~~11~~	
form 1b	91	92	93	~~11~~	
form 2a	96	97	98	~~11~~	
form 2b	101	102	103	~~11~~	
form 3a	106	107	108	~~11~~	
form 3b	111	112	113	~~11~~	
INTERCEPT 309	121	122	123	~~12~~	PTA-1156
MANGO 419	141	142	143	~~13~~	PTA-1156
INTERCEPT 429	151	152	153	~~14~~	PTA-455
TANGO 210	171	172	173	~~15~~	PTA-438
TANGO 366	191	192	193	~~16~~	PTA-424
INTERCEPT 394	201	202	203	~~17~~	PTA-424
INTERCEPT 400	221	222	223	~~18~~	PTA-438
INTERCEPT 217	271	272	273	~~19~~	PTA-147
INTERCEPT 297	279	280	281	~~20~~	PTA-147
TANGO 276	303	304	305	~~21~~	PTA-150
TANGO 292	308	309	310	~~22~~	207230
TANGO 331	324	325	326	~~23~~	PTA-147

Table A-2

Protein Designation	SEQ ID NOs			~~Depicted in Figure #~~	ATCC® Accession #
	cDNA	ORF	Protein		
TANGO 332	329	330	331	~~24~~	PTA-151
TANGO 202	371	372	373	~~25~~	207219
TANGO 234	379	380	381	~~26~~	207184
TANGO 265	387	388	389	~~27~~	207228
TANGO 286	403	404	405	~~28~~	207220
TANGO 294	415	416	417	~~29~~	207220
INTERCEPT 296	423	424	425	~~30~~	207220

Table A-3

Protein Designation	SEQ ID NOs			~~Depicted in Figure #~~	ATCC® Accession #
	cDNA	ORF	Protein		
murine INTERCEPT 289	161	162	163	~~11~~	
murine TANGO 210	181	182	183	~~15~~	
murine INTERCEPT 400	241	242	243	~~18~~	
rat INTERCEPT 400	251	252	253	~~18~~	
murine INTERCEPT 217		362	363	~~19~~	
gerbil TANGO 292	351	352	353	~~22~~	
murine TANGO 202	437	438	439	~~25~~	

Please amend the paragraph beginning on line 19 of page 284 as follows:

The determination of percent identity between two sequences can be accomplished using a mathematical algorithm. A preferred, non-limiting example of a mathematical algorithm utilized for the comparison of two sequences is the algorithm of Karlin and Altschul (1990) Proc. Natl. Acad. Sci. USA 87:2264-2268, modified as in Karlin and Altschul (1993) Proc. Natl. Acad. Sci. USA 90:5873-5877. Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul, et al. (1990) J. Mol. Biol. 215:403-410. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to a nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to a protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul et al. (1997) Nucleic Acids Res. 25:3389-3402. Alternatively, PSI-Blast can be used to perform

an iterated search which detects distant relationships between molecules (Id.). When utilizing BLAST, Gapped BLAST, and PSI-Blast programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used. ~~See http://www.ncbi.nlm.nih.gov.~~

Please amend the paragraphs beginning on line 19 of page 285 as follows:

After the path matrix is complete, the highest value on the surface of comparison represents the end of the best region of similarity between the sequences. The best path from this highest value backwards to the point where the values revert to zero is the alignment shown by BestFit. This alignment is the best segment of similarity between the two sequences. ~~Further documentation can be found at http://ir.uedavis.edu/GCGhelp/bestfit.html#algorithm.~~

Additional algorithms for sequence analysis are known in the art and include ADVANCE and ADAM as described in Torellis and Robotti (1994) Comput. Appl. Biosci., 10:3-5; and FASTA described in Pearson and Lipman (1988) Proc. Natl. Acad. Sci. 85:2444-8. Within FASTA, ktup is a control option that sets the sensitivity and speed of the search. If ktup=2, similar regions in the two sequences being compared are found by looking at pairs of aligned residues; if ktup=1, single aligned amino acids are examined. ktup can be set to 2 or 1 for protein sequences, or from 1 to 6 for DNA sequences. The default if ktup is not specified is 2 for proteins and 6 for DNA. ~~For a further description of FASTA parameters, see http://bioweb.pasteur.fr/docs/man/man/fasta.1.html#sect2, the contents of which are incorporated herein by reference.~~

Please amend the paragraph beginning on line 18 of page 302 as follows:

Examples of epitopes encompassed by the antigenic peptide are regions that are located on the surface of the protein, e.g., hydrophilic regions. Figures 1, 5, 7, 10A-10F, 12, 13, 18, 19, 20, 21, 27, 28, 29, 30, 36, 38, 40, 41, 44, 47, 48, 51, 56A-56B, 57, 62, 63, 67 and 69~~3, 8, 10G, 11Y-1 through 11Y-6, 11Z-6, 12D, 13B, 14B, 15E, 15J, 16E, 17G, 18D, 18G, 19F, 19L, 20D, 21E, 22D, 22M, 23D, 24F, 25L, 25M, 26J, 27U, 28E, 29F, and 30D~~ are hydrophobicity plots of proteins of the invention. These or similar analyses can be used to identify hydrophilic regions.